

cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a patient.

Sequence 10 AA;

Query Match 100.0%; Score 47; DB 2; Length 10;
Best Local Similarity 100.0%; Prd. No. 0.0029; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Idx 0;

Qy 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 2
AY05988 standard; peptide; 10 AA.
ID AY05988;
AC AC
XX DT 16-AUG-1999 (first entry)
XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA;
OS Homo sapiens.
PN W09918206-A2.
XX PD 15-APR-1999.
XX PP 21-SEP-1998; 98WO-US019669.
XX PR 08-OCT-1997; 97US-0061428P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Wang R, Rosenberg SA, Zeng G;
XX DR WPI; 2001-436851/54.

XX PT New NY-BSO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.
XX PS Example 6; Fig 6A; 134pp; English.
XX CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY BSO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting the growth of
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-BSO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human NY BSO-1
CC peptide used in the characterisation of the NY BSO-1 epitope recognised
CC by T84-1.
XX SQ Sequence 14 AA;
XX Query Match 100.0%; Score 47; DB 4; Length 14;

XX SQ Sequence 10 AA;
XX Query Match 100.0%; Score 47; DB 2; Length 10;
Best Local Similarity 100.0%; Prd. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Idx 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 3
AAB07788 standard; peptide; 14 AA.
ID AAB07788
AC AC
XX DT 06-NOV-2001 (first entry)
XX DR Human NY ESO-1 Peptide #22 to characterise epitope recognised by T84-1.
XX XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX OS Homo sapiens.
XX PN W020015393-A2.
XX PD 02-AUG-2001.
XX PP 26-JAN-2001; 2001WO-US002765.
XX PR 28-JAN-2000; 2000US-0179004P.
XX PR 29-SEP-2000; 2000US-0237107P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Wang R, Rosenberg SA, Zeng G;
XX DR WPI; 2001-436851/54.

XX PT New NY-BSO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.
XX PS Example 6; Fig 6A; 134pp; English.
XX CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY BSO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting the growth of
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-BSO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human NY BSO-1
CC peptide used in the characterisation of the NY BSO-1 epitope recognised
CC by T84-1.
XX SQ Sequence 14 AA;
XX Query Match 100.0%; Score 47; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0;

Qy 1 TVSGNLTIR 10
Db 4 TVSGNLTIR 13

RESULT 4

AAB07728
ID AAE07728 standard; peptide; 14 AA.
XX 06-NOV-2001 (first entry)

Human NY ESO-1 MHC class II restricted T cell epitope #14.
Human; major histocompatibility complex; MHC; vaccine; metastasis;

class II restricted T cell epitope; MHC-II epitope; cancer antigen;
NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
tumour-specific humoral-mediated immunity; cancer; cytostatic;
immunotherapy.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;

class II restricted T cell epitope; MHC-II epitope; cancer antigen;
NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;

tumour-specific humoral-mediated immunity; cancer; cytostatic;

immunotherapy.

XX Homo sapiens.

OS Homo sapiens.

XX WO200155393-A2.

PN 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US0002765.

* PR 28-JAN-2000; 2000US-0179004P.

PR 29-SEP-2000; 2000US-0237107P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,

useful as immunogen and vaccine for inhibiting cancer in a mammal or as

protection from metastasis.

XX PS Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major

histocompatibility (MHC) class II restricted T cell epitope (MHC-II

epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes

from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte

antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP

restricted. The products of the gene are promising candidates for

immunotherapeutic strategies for the prevention, treatment and diagnosis

of patients with cancer. The cancer epitopes are useful as immunogen and

vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T

lymphocytes resulting in protection of the recipient from development of

cancer and protection from metastasis, or by inhibiting the growth of

cells expressing the NY-ESO-1 gene product. The cancer peptides are also

useful as diagnostic agent to detect the presence of cancer, to enhance

the generation of antibody and/or T cell responses against any given

target antigen and/or hapten and to induce tumour-specific humoral-

mediated immunity against cancer. The present sequence is MHC class II

restricted T cell epitope of human NY ESO-1 protein

Sequence 14 AA;

CC Query Match 100.0%; Score 47; DB 4; Length 15;

CC Best Local Similarity 100.0%; Pred. No. 0.0049;

CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC SQ 1 TVSGNLTIR 10

CC Query Match 100.0%; Score 47; DB 4; Length 14;

CC Best Local Similarity 100.0%; Pred. No. 0.0049;

CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC SQ 1 TVSGNLTIR 10

CC Query Match 100.0%; Score 47; DB 4; Length 15;

CC Best Local Similarity 100.0%; Pred. No. 0.0049;

CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC SQ 1 TVSGNLTIR 10

DB 4 TVSGNLTIR 13

RESULT 5

AAB07726

ID AAE07726 standard; peptide; 15 AA.

XX AC AAB07726;

XX DT 06-NOV-2001 (first entry)

XX DE Human NY ESO-1 MHC class II restricted T cell epitope #12.

XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;

XX KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;

XX KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;

XX KW tumour-specific humoral-mediated immunity; cancer; cytostatic;

XX KW immunotherapy.

XX Homo sapiens.

OS Homo sapiens.

XX WO200155393-A2.

PN 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US0002765.

* PR 28-JAN-2000; 2000US-0179004P.

PR 29-SEP-2000; 2000US-0237107P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,

useful as immunogen and vaccine for inhibiting cancer in a mammal or as

protection from metastasis.

XX PS Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major

histocompatibility (MHC) class II restricted T cell epitope (MHC-II

epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes

from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte

antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP

restricted. The products of the gene are promising candidates for

immunotherapeutic strategies for the prevention, treatment and diagnosis

of patients with cancer. The cancer epitopes are useful as immunogen and

vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T

lymphocytes resulting in protection of the recipient from development of

cancer and protection from metastasis, or by inhibiting the growth of

cells expressing the NY-ESO-1 gene product. The cancer peptides are also

useful as diagnostic agent to detect the presence of cancer, to enhance

the generation of antibody and/or T cell responses against any given

target antigen and/or hapten and to induce tumour-specific humoral-

mediated immunity against cancer. The present sequence is MHC class II

restricted T cell epitope of human NY ESO-1 protein

Sequence 14 AA;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 15

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

ID AAE07727 standard; peptide; 15 AA.
 XX
 AC AAE07727;
 XX DE Human NY ESO-1 peptide #20 to characterise epitope recognised by TE4-1.
 XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 DT 06-NOV-2001 (first entry)
 XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 DE Human NY ESO-1 MHC class II restricted T cell epitope #13.
 XX NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
 DE immunotherapy.
 XX Homo sapiens.
 OS EN WO200155393-A2.
 XX PD 02-AUG-2001.
 XX PP 26-JAN-2001; 2001WO-US002765.
 XX PR 28-JAN-2000; 2000US-017904P.
 PD 29-SEP-2000; 2000US-023710P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Wang R, Rosenberg SA, Zeng G;
 XX DR WPI; 2001-496851/54.
 XX PT New NY ESO cancer peptide or MHC class II restricted T cell epitopes,
 XX useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 protection from metastasis.
 XX PS Example 6; Fig 6A; 134pp; English.
 XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) Class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC peptide used in the characterisation of the NY ESO-1 epitope recognised
 CC by TR4-1.
 XX Sequence 15 AA:
 SQ Query Match 1 TVSGNLTIR 10
 Best Local Similarity 100 %; Score 47; DB 4; Length 15;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YY 1 TVSGNLTIR 10
 DB 5 TVSGNLTIR 14
 RESULT 8
 AAE07786
 ID AAE07786 standard; peptide; 15 AA.
 XX DE 06-NOV-2001 (first entry)
 DB Human NY ESO-1 peptide #21 to characterise epitope recognised by TE4-1.
 AC AAE07786;
 XX DT 06-NOV-2001 (first entry)
 DE Human; major histocompatibility complex; MHC; vaccine; metastasis;

Class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 tumour-specific humoral-mediated immunity; cancer; cytostatic;
 immunotherapy.

XX OS Homo sapiens.

XX PN WO200155333-A2.

XX PD 02-AUG-2001.

XX PR 26-JAN-2001; 2001WO-US002765.

XX PR 28-JAN-2000; 2000US-0179004P.

XX PR 29-SEP-2000; 2000US-0237107P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX PS Example 6: FIG 6A; 134PP; English.

XX PT The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cells expressing the NY-ESO-1 gene product. The cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope recognised by TE4-1

XX Sequence 15 AA:

XX Query Match 100.0%; Score 47; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.0049;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ

OS Synthetic.

OS Homo sapiens.

XX PN WO953938-A1.

XX PD 28-OCT-1999.

XX PP 24-MAR-1999; 9910-US006875.

XX PR 17-APR-1998; 98US-00062422.

XX PR 02-OCT-1998; 98US-0016546.

XX PA (LUDWIG) LUDWIG INST CANCER RES.

XX PI Stockert E, Jager B, Chen Y, Scanlan M, Alexander K, Old LJ;

XX PI Gure A, Ritter G;

XX DR WPI; 2000-038483/03.

XX PT Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.

XX PS Claim 4; Page 22; 49PP; English.

CC Peptides #B-#13 (AYA52435-Y52440) are peptides derived from the human tumour antigen, NY-ESO-1 (AYA52430) which can bind to MHC major histocompatibility Class II HLA-DR53 molecules, thereby stimulating proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially isolated from an oesophagus squamous cell cancer cDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens with expression in other tumour types being sporadic. These NY-ESO-1-derived peptides may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or CC lymphoma) and to stimulate the proliferation of T cells

CC Sequence 18 AA;

CC Query Match 100.0%; Score 47; DB 3; Length 18;

CC Best Local Similarity 100.0%; Pred. No. 0.0062;

CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC SQ

XX 1 TVSGNLTIR 10

XX ||||| | | | | | | | |

XX 1 TVSGNLTIR 10

XX

XX Query Match 100.0%; Score 47; DB 3; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 0.0062;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ

XX 1 TVSGNLTIR 10

XX ||||| | | | | | | | |

XX 1 TVSGNLTIR 10

XX

XX RESULT 10

XX AAB69940

XX ID AAB69940 standard; peptide; 18 AA.

XX AC AAB69940;

XX DT 27-APR-2001 (first entry)

XX Human tumour antigen NY-ESO-1 peptide #13.

XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;

XX T-cell; helper; stimulation; treatment; diagnosis;

XX prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;

XX hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.

XX PN WO200107917-A1.

XX ID 01-FEB-2001.

XX PR 14-JUL-2000; 2000WO-US019220.

XX XX

PR 23-JUL-1999; 99US-00359503.

XX (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scarlan M;
PI; 2001-182822/18.

Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.

Example 16; Page 27; 50pp; English.

The present sequence is given in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder carcinoma

SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

46 RESULT 11

AB69944 Human NY-ESO-1 standard, peptide: 18 AA.
ID AA69944
AC AA69944;
XX 27-APR-2001 (First entry)

DE Human NY-ESO-1 HLA-DR53 binding motif #6.
XX KX Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX CS Homo sapiens.
PN WO200105917-A1.
XX PD 01-FEB-2001.

PP 14-JUL-2000; 2000WO-US019220.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.

XX PR Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scarlan M;
XX PI; 2001-182822/18.

Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.

Example 16; Page 28; 50pp; English.

The present sequence is given in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder carcinoma

SQ Sequence 18 AA;

47 RESULT 12

AAU01544 AAU01544 standard; peptide: 18 AA.

ID AAU01544
AC AAU01544;
XX DT 18-JUL-2001 (First entry)

DB HLA-DR53 recognising NY-ESO-1 peptide #6.

XX Qy 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 13

AAU01544 Human NY-ESO-1 tumour rejection antigen precursor; SSX-2; MHC Class II;

ID AAU01544
AC AAU01544;
XX DT 18-JUL-2001 (First entry)

DB NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;

XX KW major histocompatibility complex; helper T cell; HLA-DR; cancer;

KW human leukocyte antigen-determining region; disease progression;

KW disease regression; disease onset; body tissue; body fluid; enzyme label;

KW radioactive label; monoclonal antibody.

XX QS Homo sapiens.

XX PN WO200123560-A2.

XX PD 05-APR-2001.

XX PF 26-SEP-2000; 2000WO-US026411.

XX PR 29-SEP-1999; 99US-00400036.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Tureci O, Sahin U, Pfreundschuh M;

XX DR WPI; 2001-266156/27.

XX PT Polypeptides binding to major histocompatibility complex class III human

KW leukocyte antigen-determining region molecule having amino acid sequence

KW found in tumor rejection antigen precursor used for stimulating

KW proliferation of helper T cells.

XX PS Example 13; Page 19; 62pp; English.

XX CC The sequence represents a human NY-ESO-1 tumour rejection antigen

CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and

CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility

CC complex (MHC) Class II molecules such as human leucocyte antigen-

CC determining region (HLA-DR) molecules and stimulate proliferation of

helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoreactive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the complex.

CC sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 13
AAU01540 standard; peptide; 18 AA.

ID AAU01540
XX DT 18-JUL-2001 (first entry)

XX DE HLA-DR53 recognising NY-ESO-1 peptide #2.

XX AC AAU01540;

XX XX major histocompatibility complex; helper T cell; HLA-DR; cancer;

XX KW human leukocyte antigen-determining region; disease progression;

XX KW disease regression; disease onset; body tissue; body fluid; enzyme label;

XX radioactive label; monoclonal antibody.

OS Homo sapiens.

PN WO200123560-A2.

XX PR 05-APR-2001.

XX PF 26-SEP-2000; 2000WO-US026411.

XX PR 29-SEP-1999; 99US-00408036.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Tureci O, Sahin U, Pfreundschuh M;

DR WPI; 2001-26156/27.

XX Polypeptides binding to major histocompatibility complex class II human

PT leukocyte antigen-determining region molecule having amino acid sequence

PT found in tumor rejection antigen precursor used for stimulating

PT proliferation of helper T cells.

XX Example 13; Page 19; 62pp; English.

PT The sequence represents a human NY-ESO-1 tumour rejection antigen-XX

CC precursor fragment which recognises and binds to HLA-DR3. NY-ESO-1 and

CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility

CC complex (MHC) Class II molecules and stimulate proliferation of

CC helper T cells. The peptides can be administered to an HLA-DR positive

CC cell in order to stimulate the helper T cells. An MHC Class II HLA-DR-

CC NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in

CC free form is useful for this stimulation. The nucleic acid is useful for

CC screening for a cancerous condition, which involves contacting a subject
CC sample to a cell line transfected with the immunoreactive cell (helper T
CC cell), where interaction is indicative of cancer. In addition, a sample
CC from a patient (for example, a body fluid or tissue) can be monitored for
CC the amount of the complex present in the bloodstream. This is useful for
CC determining regression, progression or onset of a cancerous condition.
CC The method involves contacting the sample with a radioactive labelled or
CC enzyme labelled monoclonal antibody which specifically binds with the
CC complex.

XX Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 14
ID AAB07769 standard; peptide; 18 AA.

XX XX AAB07769;
XX AC AAB07769;

XX DT 06-NOV-2001 (first entry)

XX DE Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.

XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;

XX KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;

XX KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;

XX KW tumour-specific humoral-mediated immunity; cancer; cytostatic;

XX KW immunotherapy.

OS Homo sapiens.

DN WO200155393-A2.

XX PD 02-AUG-2001.

XX PF 26-JAN-2001; 2001WO-US002765.

XX PR 28-JAN-2000; 2000US-0179004P.

PR 29-SEP-2000; 2000US-0237107P.

XX PA (TSSH) US DEPT HEALTH & HUMAN SERVICES.

XX XX Wang R, Rosenberg SA, Zeng G;

XX DR WPI; 2001-496851/54.

XX PT New NY-ESO cancer Peptide or MHC class II restricted T cell epitopes,

PT useful as immunogen and vaccine for protecting cancer in a mammal or as

PT protection from metastasis.

XX Claim 84; Page 84; 134pp; English.

XX The invention relates to the identification and isolation of major

CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II

CC epitope), derived from the cancer antigen, NY ESO-1. The MHC-II epitopes

CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte

CC antigen (HLA) class II restricted manner. In Particular HLA-DR or HLA-DP

CC restricted. The products of the gene are promising candidates for

CC immunotherapeutic strategies for the prevention, treatment and diagnosis

CC of patients with cancer. The cancer epitopes are useful as immunogen and

CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T

CC lymphocytes resulting in protection of the recipient from development of

CC cancer and protection from metastasis, or by inhibiting the growth of

CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also

CC useful as diagnostic agent to detect the presence of cancer, to enhance

the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1 HLA DR restricted T cell cancer peptide.

XX Sequence 18 AA;
 SQ Query Match 100.0%; Score 47; DB 4; Length 18;
 Best Local Similarity 100.0%; Prod. No. 0.0062;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TVSGNTLIR 10
 ||||| | | | |
 Db 7 TVSGNTLIR 16

RESULT 15
 ID AAE07742 standard; peptide; 20 AA.
 XX AAE07742;
 XX DT 06-NOV-2001 (first entry)
 XX Human ESO p125-145 peptide, to identify MHC class II-restricted epitopes.
 XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 XX Class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 XX NY ESO-1 Protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 XX tumour-specific humoral-mediated immunity; cancer; cytotoxic;
 XX immunotherapy.
 XX CS Homo sapiens.
 XX PN WO200155393-A2.
 XX PD 02-AUG-2001.
 XX PP 26-JAN-2001; 2001WQ-US062765.
 XX PR 28-JAN-2000; 2000US-0179004P.
 XX PR 29-SEP-2000; 2000US-023107P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Wang R, Rosenberg SA, Zeng G;
 XX DR WPI: 2001-496651/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.

XX PS Example 3; Fig 3; 134pp; English.

XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human ESO p126-
 CC 145 peptide used in the identification of putative MHC class II -
 CC restricted epitopes from HLA-DR4-transgenic mice

XX SQ Sequence 20 AA;
 XX Query Match 100.0%; Score 47; DB 4; Length 20;
 XX Best Local Similarity 100.0%; Prod. No. 0.0011;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TVSGNTLIR 10
 ||||| | | | |
 Db 2 TVSGNTLIR 11

Search completed: June 22, 2004, 08:51:24
 Job time : 34.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 22, 2004, 08:49:38 : Search time 11 Seconds

(without alignments)

46.933 Million cell updates/sec

Title: US-09-529-206D-4_COPY_127_136

Perfect score: 47

Sequence: 1 TVGZNLTIR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%

Listing First 45 summaries

Database : Issued Patents API:
 1: /cgna2_6/ptodata/2/iaa/5a/COMB.pep.*
 2: /cgna2_6/ptodata/2/iaa/5b/COMB.pep.*
 3: /cgna2_6/ptodata/2/iaa/65_-COMB.pep.*
 4: /cgna2_6/ptodata/2/iaa/66_COMB.pep.*
 5: /cgna2_6/ptodata/2/iaa/PECTUS_COMB.pep.*
 6: /cgna2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	47	100	18	US-09-359-003-9
2	47	100	18	US-09-359-003-13
3	47	100	180	US-08-791-495-9
4	47	100	180	US-08-163B-8
5	47	100	180	US-09-751-798-8
6	47	100	180	US-09-392-014-25
7	42	89	9	US-09-344-040C-125
8	42	89	9	US-09-833-039A-125
9	38	80	9	US-09-344-040C-120
10	38	80	9	US-09-833-039A-120
11	38	80	9	US-08-91-95-7
12	74	5	342	US-09-134-001C-248
13	72	3	149	US-09-540-236-2614
14	34	72	3	US-09-132-10-1076
15	33	70	97	US-08-118-70-329
16	33	70	97	PCT-US93-00528-129
17	33	70	109	US-09-341-461-35
18	33	70	362	US-09-134-001C-209
19	33	70	379	US-08-118-70-32
20	33	70	379	PCT-US93-00528-32
21	33	70	470	US-09-292-071-25
22	33	70	470	US-09-292-069A-25
23	33	70	470	US-09-767-013-25
24	33	70	470	US-09-292-072-25
25	33	70	471	US-07-817-020-8
26	33	70	471	US-07-996-072A-11
27	33	70	471	US-08-370-542-7

Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 11, Appli
Sequence 14, Appli
Sequence 17, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 122, Appli
Sequence 228, Appli
Sequence 8, Appli
Sequence 31, Appli
Sequence 33, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-9
Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; TITLE OF INVENTION: Method for Determining Status of A
; Cancersous Condition By Determining Antibodies
; to NY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Falbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 625163man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

TOPOLOGY: linear

US-09-359-503-9

Query Match 100.0%; Score 47; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.008; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

Db 7 TVSGNLTIR 16

RESULT 2

US-09-359-503-13

Query Match 100.0%; Application US/09359503

Patent No. 6251603

GENERAL INFORMATION:

APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;

TITLE OF INVENTION: Method for Determining Status of A

TITLE OF INVENTION: Cancerous Condition By Determining Antibodies

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski, L.L.P.

STREET: 666 Fifth Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/359,503

FILING DATE: July 23, 1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/165,546

FILING DATE: October 2, 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/062,422

FILING DATE: April 17, 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/937,263

FILING DATE: September 15, 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/752,182

FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6231603man D.

REGISTRATION NUMBER: 30,946

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000

TELEFAX: (212) 752-5358

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-09-359-503-13

Query Match 100.0%; Score 47; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.008; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

Db 1 TVSGNLTIR 10

RESULT 3

US-08-791-495-9

Sequence 9, Application US/08791495

Patent No. 5811519

GENERAL INFORMATION:

APPLICANT: Letch, Bernard

APPLICANT: Lucas, Sophie

APPLICANT: De Smet, Charles

APPLICANT: Godelaine, Danielle

APPLICANT: Bonc-Palleur, Thierry

TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEES: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

COUNTRY: MA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/791,495

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Van Amsterdam, John R.

REGISTRATION NUMBER: 40,212

REFERENCE/DOCKET NUMBER: L0461/7005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 180 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-791-495-9

Query Match 100.0%; Score 47; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

Db 127 TVSGNLTIR 136

RESULT 4

US-08-337-263B-8

Sequence 8, Application US/08937263B

Patent No. 6274145

GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;

APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;

APPLICANT: Alexander, Kruth; Drijfhout, Jan W.

TITLE OF INVENTION: ISOLATED NUCLEAR ACID MOLECULE

TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN,

THE ANTIGEN

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEES: Fulbright & Jaworski, L.L.P.

STREET: 666 Fifth Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10105

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,263B
 FILING DATE: September 15, 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/725,182
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Sinn, Eric, Patent Agent
 REGISTRATION NUMBER: 40,177
 REFERENCE/DOCKET NUMBER: LUD 5466.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-1000
 TELEX/FAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-937-263B-8

Query Match 100.0%; Score 47; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Missmatches 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 5
 US-09-751-798-8
 Sequence 8, Application: US/09751798
 GENERAL INFORMATION:
 PATENT NO. 654177
 APPLICANT: Stockert, Elisabeth; Jager, Elke;
 APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
 APPLICANT: Knuth, Alexander; Old, Lloyd J.
 TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
 TITLE OF INVENTION: Associated Proteins, Uses Thereof,
 TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
 TITLE OF INVENTION: Binding Peptides Derived Therefrom
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103

PRIOR APPLICATION DATA:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/751,798
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/062,422
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 652177man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-2168

RESULT 6
 US-09-392-714-25
 Sequence 25, Application US/09392714A
 Patent No. 6686147
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Matthew J.
 APPLICANT: Gure, Ali O.
 APPLICANT: Williamson, Barbara
 APPLICANT: Chen, Yao-Tseng
 APPLICANT: Old, Lloyd J.
 TITLE OF INVENTION: Cancer Associated Antigens and Uses
 NUMBER OF SEQ ID NOS: 30
 FILE REFERENCE: L0461/7062
 CURRENT APPLICATION NUMBER: US/09/392,714A
 CURRENT FILING DATE: 1999-09-09
 EARLIER APPLICATION NUMBER: PCT/US98/14679
 EARLIER FILING DATE: 1998-07-15
 NUMBER OF SEQ ID NOS: 30
 SEQ ID NO: 25
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-392-714-25

Query Match 100.0%; Score 47; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Missmatches 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 7
 US-09-344-040C-125
 Sequence 125, Application US/09344040C
 GENERAL INFORMATION:
 PATENT NO. 6548064
 APPLICANT: Turci, Ozlem
 APPLICANT: Sabin, Ugur
 APPLICANT: Pfreundschuh, Michael
 APPLICANT: Rameesee, Hans Georg
 APPLICANT: Stevanovic, Stefan
 TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Expression of an SSX Gene
 TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
 CURRENT APPLICATION NUMBER: US/09/344,040C
 CURRENT FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: US 09/105,839
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: US 08/851,130
 PRIOR FILING DATE: 1997-05-05
 NUMBER OF SEQ ID NOS: 132
 SEQ ID NO: 125

LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-344-040C-125

Query Match 89.4%; Score 42; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 TVSGNLTI 9
 Db 1 TVSGNLTI 9

RESULT 8
 US-09-833-039A-125
 ; Sequence 125, Application US/09833039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; TITLE OF INVENTION: Peptide and Uses Thereof
 ; FILE REFERENCE: LUD 5622.1
 ; CURRENT APPLICATION NUMBER: US/09/833,039A
 ; CURRENT FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: US 09/409,455
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/344,040
 ; PRIOR FILING DATE: 1999-06-26
 ; PRIOR APPLICATION NUMBER: US 09/105,839
 ; PRIOR FILING DATE: 1998-06-26
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 125
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-833-039A-125

Query Match 89.4%; Score 42; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 TVSGNLTI 9
 Db 1 TVSGNLTI 9

RESULT 9
 US-09-344-040C-120
 ; Sequence 120, Application US/09344040C
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
 ; FILE REFERENCE: LUD 5556.1
 ; CURRENT FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US/09/344,040C
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 08/851,130
 ; NUMBER OF SEQ ID NOS: 132
 ; LENGTH: 9
 ; TYPE: PRT

Query Match 80.9%; Score 38; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 TVSGNLTI 8
 Db 2 TVSGNLTI 9

RESULT 10
 US-09-833-039A-120
 ; Sequence 120, Application US/09833039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; TITLE OF INVENTION: Peptide and Uses Thereof
 ; FILE REFERENCE: LUD 5622.1
 ; CURRENT APPLICATION NUMBER: US/09/833,039A
 ; CURRENT FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: US 09/409,455
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/344,040
 ; PRIOR FILING DATE: 1999-06-26
 ; PRIOR APPLICATION NUMBER: US 09/105,839
 ; PRIOR FILING DATE: 1998-06-26
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 120
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-833-039A-120

Query Match 80.9%; Score 38; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 TVSGNLTI 8
 Db 2 TVSGNLTI 9

RESULT 11
 US-09-791-495-7
 ; Sequence 7, Application US/08791495
 ; Patent No. 5811519
 ; GENERAL INFORMATION:
 ; APPLICANT: Letch, Bernard
 ; APPLICANT: Lucas, Sophie
 ; APPLICANT: De Smet, Charles
 ; APPLICANT: Godalaine, Danielle
 ; APPLICANT: Bon-Falleur, Thierry
 ; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; ZIP: 02210
 ; COUNTRY: USA
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/791,495

FILING DATE: US-09-540-236-2614

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Van Amsterdam, John R.

REGISTRATION NUMBER: 40,212

REFERENCE/DOCKET NUMBER: J0461/7005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 180 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-791-495-7

Query Match 80.9%; Score 38; DB 2; Length 180;

Best Local Similarity 80.0%; Pred. No. 5.8;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

Db 127 TVSGNLFIR 136

RESULT 12

US-09-134-001C-5428

Sequence 5428, Application US/09134001C

GENERAL INFORMATION:

Patent No. 6380370

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

PRIOR APPLICATION NUMBER: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 342

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-5428

Query Match 74.5%; Score 35; DB 4; Length 342;

Best Local Similarity 70.0%; Pred. No. 4.6;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

Db 251 TVGGNIMKIR 260

RESULT 13

US-09-540-236-2614

Sequence 2614, Application US/09540226

GENERAL INFORMATION:

Patent No. 6673910

APPLICANT: Gary L. Bretton et al.

TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAL

FILE REFERENCE: 2709 2005-001

CURRENT APPLICATION NUMBER: US/09/540,226

CURRENT FILING DATE: 2006-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO: 2614

LENGTH: 149

TYPE: PRT

ORGANISM: M.catarrhalis

US-09-540-236-2614

Query Match 72.3%; Score 34; DB 4; Length 149;

Best Local Similarity 60.0%; Pred. No. 28;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

Db 129 TVGNTTITK 138

RESULT 14

US-09-732-210-1076

Sequence 1076, Application US/09732210

GENERAL INFORMATION:

Patent No. 6573361

APPLICANT: Bunkers, Greg J.

APPLICANT: Liang, Jihong

APPLICANT: Mittane, Cindy A.

APPLICANT: Seale, Jeffrey W.

APPLICANT: Wu, Yonnie S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use

FILE REFERENCE: 38-21(15036)B

CURRENT APPLICATION NUMBER: US/09/732,210

CURRENT FILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/169,513

PRIOR FILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: US 60/169,340

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO: 1076

LENGTH: 177

TYPE: PRT

ORGANISM: Bacillus stearothermophilus

US-09-732-210-1076

Query Match 72.3%; Score 34; DB 4; Length 177;

Best Local Similarity 55.6%; Pred. No. 34;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 9

Db 43 TVGNTVITY 51

RESULT 15

US-09-118-270-329

Sequence 329, Application US/08118270

GENERAL INFORMATION:

Patent No. 5500384

APPLICANT: Murphy, Randall B.

APPLICANT: Schuster, David I.

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWNDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/118,270

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/118,270

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34033
REFERENCE DOCUMENT NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3228
TELEX: 248633
INFORMATION FOR SEQ ID NO: 329:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-329

Query Match Similarity 70.2%; Score 33; DB 1; Length 97;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TVSGNLTI 9
Db 17 TIAGNLYI 25

Search completed: June 22, 2004, 08:54:48
Job time : 11 secs

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19	42	89.4	10	15	US-10-117-937-186
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23	38	80.9	180	12	US-10-236-734-834
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33	34	72.3	49	12	US-10-124-599-174030
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36	34	72.3	299	14	US-10-060-79B-6
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39	34	72.3	585	12	US-10-232-224-242
40	34	72.3	585	14	US-10-227-884-242
41	34	72.3	585	14	US-10-310-153-242
42	34	72.3	585	14	US-10-230-338-242
43	34	72.3	585	14	US-10-218-631-242
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Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0%				
Maximum Match 100%					
Listing First 45 summaries					
Published Applications:	*				
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	Score	Match %	Length		
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2	4.7	100.0	20	15	US-10-164-08A-34
3	4.7	100.0	30	12	US-10-296-734-144
4	4.7	100.0	54	16	US-10-447-111-140
5	4.7	100.0	180	9	US-09-731-798-8
6	4.7	100.0	180	10	US-09-B49-652-30
7	4.7	100.0	180	12	US-10-296-734-832
8	4.7	100.0	180	13	US-10-023-132-8
9	4.7	100.0	180	14	US-10-107-655-71
10	4.7	100.0	180	15	US-10-026-066-3
11	4.7	100.0	180	15	US-10-117-937-74
12	4.7	100.0	180	15	US-10-925-057-386
13	4.7	100.0	180	16	US-0-188-832-139
14	4.7	100.0	175	9	US-09-831-882-27
15	4.7	100.0	1541	12	US-10-296-734-1454

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Query Match      100.0%; Score 47; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0319;
Matches 10; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

Qy      1 TVSGNLTIR 1.0
        ||||| | |
Db      9 TVSGNLTIR 1.8

RESULT 2
US 10-164-078A-34
; Sequence 34, Application US/10164078A
; Publication No. US20030228323A1
; GENERAL INFORMATION:
; APPLICANT: Blisborough, Janine
;           Schultz, Erwin
; APPLICANT: Panichelli, Christopherne
; APPLICANT: 

```

Page 2

Publication No. US20030165834A1
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Matthew J.
 APPLICANT: Old, Lloyd J.
 APPLICANT: Stochert, Elisabeth
 TITLE OF INVENTION: Colon Cancer Antigen Panel
 FILE REFERENCE: L04617105 (JRV)
 CURRENT APPLICATION NUMBER: US09/849,602
 CURRENT FILING DATE: 2001-05-04
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 30
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-849-602-30

Query Match 100.0%; Score 47; DB 10; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 7
 US-10-296-734-832
 ; Sequence 832, Application US/10296734
 ; Publication No. US2004005413A1
 GENERAL INFORMATION:
 APPLICANT: Thompson, Scott A
 APPLICANT: Ramshaw, Ian A
 TITLE OF INVENTION: Synthetic molecules and uses therefor
 FILE REFERENCE: Savine
 CURRENT APPLICATION NUMBER: US/10/296,734
 CURRENT FILING DATE: 2003-08-04
 PRIOR APPLICATION NUMBER: AU PQ7761/00
 PRIOR FILING DATE: 2000-05-26
 NUMBER OF SEQ ID NOS: 1507
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 832
 LENGTH: 180
 TYPE: PRT
 OTHER INFORMATION: NYNS01a consensus polypeptide

US-10-296-734-832

Query Match 100.0%; Score 47; DB 12; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 8
 US-10-023-182-8
 ; Sequence 8, Application US/10023182
 ; Publication No. US20020164655A1
 GENERAL INFORMATION:
 APPLICANT: Stockert, Elisabeth; Jager, Blke;
 Chen, Yao-tseng; Scanlan, Matthew;
 Knut, Alexander; Old, Lloyd J.
 TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
 Associated Proteins, Uses Thereof,
 Truncated Forms of NY-ESO-1, and HLA
 Binding Peptides Derived Therefrom
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:

ADDRESS: Fulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/023,182
 FILING DATE: 17-Dec-2001
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/751,798
 FILING DATE: December 29, 2000
 APPLICATION NUMBER: 09/062,122
 FILING DATE: <Unknown>
 APPLICATION NUMBER: 08/725,182
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. US20020164665A1man, D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3168
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-10-023-182-8

Query Match 100.0%; Score 47; DB 13; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 9
 US-10-207-655-71
 ; Sequence 71, Application US/10207655
 ; GENERAL INFORMATION:
 PUBLIC "-//IETF//DTD SGML//EN//NO"
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Hayden-Ledbetter, Martha S.
 ; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
 ; FILE REFERENCE: 390069.401C1
 ; CURRENT APPLICATION NUMBER: US/10/207,655
 ; NUMBER OF SEQ ID NOS: 426
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 71
 ; LENGTH: 180
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-207-655-71

Query Match 100.0%; Score 47; DB 14; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 10
 US-10-026-066-3
 Sequence 3, Application US/10026066
 Publication No. US20030215425A1
 GENERAL INFORMATION:
 APPLICANT: Simard, John J. E.
 TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
 FILE REFERENCE: CTLIIM 21CPC1
 CURRENT APPLICATION NUMBER: US/10/026, 066
 CURRENT FILING DATE: 2001-12-07
 PRIOR APPLICATION NUMBER: 09/561, 074
 PRIOR FILING DATE: 2000-04-18
 PRIOR APPLICATION NUMBER: 09/560, 465
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 09/561, 572
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 09/561, 571
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: PCT/US01/13806
 PRIOR FILING DATE: 2001-04-27
 NUMBER OF SEQ ID NOS: 89
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 3
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-026-066-3

Query Match 100.0%; Score 47; DB 15; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36%;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 3

Qy 1 TVSGNLTIR 10
 * Db 127 TVSGNLTIR 136

RESULT 11
 US-10-117-937-74
 Sequence 74, Application US/10117937
 Publication No. US20030220239A1
 GENERAL INFORMATION:
 APPLICANT: CTL IMMUNO THERAPIES CORP.
 SIMARD, John, J.L.
 APPLICANT: DIAMOND, David, C.
 APPLICANT: LIU, Liping
 APPLICANT: XIE, Zhidong
 TITLE OF INVENTION: EPITOPE SEQUENCES
 FILE REFERENCE: CTLIIM.027A

CURRENT APPLICATION NUMBER: US/10/117, 937
 CURRENT FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: US 60/282, 211
 PRIOR FILING DATE: 2001-04-06
 PRIOR APPLICATION NUMBER: US 60/337, 017
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: US 60/363, 210
 PRIOR FILING DATE: 2002-03-07
 NUMBER OF SEQ ID NOS: 602
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 74
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-117-937-74

Query Match 100.0%; Score 47; DB 15; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36%;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 74

Qy 1 TVSGNLTIR 10
 * Db 127 TVSGNLTIR 136

RESULT 12
 US-10-95-027-386
 Sequence 386, Application US/10295027
 Publication No. US20030232350A1
 GENERAL INFORMATION:
 APPLICANT: Aziz, Natasha
 Ginsberg, Wendy M.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Glynn, Richard
 APPLICANT: Heverzi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: Eos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 Methods of Screening for Modulators of Cancer
 FILE REFERENCE: 018501-012500US
 CURRENT APPLICATION NUMBER: US/10/295, 027
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663, 733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350, 665
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335, 394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332, 464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334, 393
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: US 60/340, 376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347, 211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347, 349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355, 250
 PRIOR FILING DATE: 2002-02-08
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 386
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-295-027-386

Query Match 100.0%; Score 47; DB 15; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36%;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 * Db 127 TVSGNLTIR 136

RESULT 13
 US-10-188-832-139
 Sequence 139, Application US/10188832
 Publication No. US20040076955A1
 GENERAL INFORMATION:
 APPLICANT: Aziz, Natasha
 APPLICANT: Eos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
 and Methods of Screening for Modulators of Bladder
 TITLE OF INVENTION: Cancer
 FILE REFERENCE: 018501-002330US

Qy 1 TVSGNLTIR 10

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; CURRENT APPLICATION NUMBER: US/10/188, 832
; PRIOR APPLICATION NUMBER: US 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302, 814
; PRIOR APPLICATION NUMBER: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310, 099
; PRIOR FILING DATE: 2001-08-03
; PRIOR FILING DATE: 2001-08-03
; PRIOR FILING DATE: 2001-11-08
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2002-04-12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 47; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 127 TVSGNLTIR 136

```

```

RESULT 14
US-09-821-883-27
; Sequence 27, Application US/09821883
; Patent No. US200611310A1
; GENERAL INFORMATION:
; APPLICANT: Laius, Reiner
; APPLICANT: Vidovic, Damir
; APPLICANT: Graddis, Thomas
; TITLE OF INVENTION: Compositions and Methods for Dendritic
; Cell-Based Immunotherapy
; FILE REFERENCE: 7636-0022-30
; CURRENT APPLICATION NUMBER: US/09/821,883
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,504
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NY-ESO-1C tumor antigen
US-09-821-883-27

```

```

Query Match 100.0%; Score 47; DB 9; Length 397;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 127 TVSGNLTIR 136

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RESULT 15
US-10-296-734-1454
; Sequence 1454, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A.
; APPLICANT: Ramsaw, Ian A.
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:48:03 ; Search time 9 Seconds
(without alignments)

Title: US-09-529-206D-4_COPY_127_136
Perfect score: 47

Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:
1: piri:
2: piri2:
3: piri3:
4: piri4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	76.6	245	2 T13099	major tail protein
2	36	76.6	323	2 AD2753	lipoic Acid Synthe
3	36	76.6	323	2 B97534	lipoic acid synthe
4	35	74.5	335	2 A89837	hypothetical prote
5	34	72.3	177	1 F5BSOF	ribosomal protein
6	34	72.3	244	2 T41234	translation initia
7	34	72.3	311	2 AB3218	2-hydroxyacid dehy
8	34	72.3	314	2 G86835	hypothetical prote
9	34	72.3	1266	2 A85989	hypothetical prote
10	34	72.3	1266	2 F91143	tail fiber protein
11	33	70.2	144	1 TPBPPI	gene R protein - B
12	33	70.2	144	2 S18683	MAT3 efflux family
13	33	70.2	411	2 B95241	hypothetical prote
14	33	70.2	426	2 B98106	hypothetical prote
15	33	70.2	428	2 F85253	probable amino-acid
16	33	70.2	436	2 A81977	N-acetylglutamate
17	33	70.2	436	2 B81033	serotonin receptor
18	33	70.2	449	2 S02011	serotonin receptor
19	33	70.2	471	2 A34863	5-hydroxytryptamin
20	33	70.2	471	2 S40689	serotonin receptor
21	33	70.2	471	2 S11280	serotonin receptor
22	33	70.2	471	2 A43956	hypothetical prote
23	33	70.2	876	2 E96674	probable TMV resis
24	33	70.2	918	2 F71405	hypothetical prote
25	33	70.2	1996	2 C86898	probable integral
26	32	68.1	102	2 A81972	conserved hypothet
27	32	68.1	121	2 D81029	5-HT2 receptor -
28	32	68.1	135	2 I37105	
29	32	68.1	187	2	

RESULT 1

T13099

major tail protein V - phage N15

N;Alternate name: Protein qpl3

C;Species: Phage N15

C;Date: 13-Aug-1999 #Sequence_revision 13-Aug-1999 #text_change 13-Aug-1999

C;Accession: T13099

R:Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.B.; Smirnov, I.K.

submitted to the EMBL Data Library, May 1998

A;Reference number: 217603

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-245 <HEN>

A;Cross references: EMBL:AF064539; NID:93192683; PID:93192697; PIDN: AAC19050.1

A;Note: Gene 13

C;Superfamily: phage lambda major tail protein V

Query	Match	Similarity	Score	DB 2;	Length
QY	1 TVSGNLTIR 9	76.6%	76	DB 2;	Length 245;
Db	209 TVSGNLTIV 217	77.8%	77	Best Local Similarity	Matches 7;
		Prod. No. 13;	1;	Mismatches	Indels 0;
			1;	Gaps	0;

RESULTS 2

AD2753 Lipoc Acid Synthetase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Accession: AD2753 C;Accession: AD2753 C;Accession: AD2753 R:Rod, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. erge, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, F.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001. A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Gordon-Kamm, ster, B.W. A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:2160850; PMID:1143193 A;Accession: AD2753 A;Preliminary A;Molecule type: DNA A;Residues: 1-323 <KTR> A;Cross references: GB:AE008688; PIDN:AA142442.1; SID:2160850; PMID:1143193 A;Experimental source: strain C58 (Dupont) C;Genetics: A;Gene: lipa A;Map position: circular chromosome C;Superfamily: lipoic acid synthase

ribosomal protein L6 - *Bacillus stearothermophilus*
 N;Alternate names: ribosomal protein BL10
 C;Species: *Bacillus stearothermophilus*
 C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 12-Jun-2003
 C;Accession: A02766; B39085; S59061
 R;Kimura, M.; Rawlings, N.; Appelt, K.
 FEBS Lett. 136, 58-61, 1981
 A;Title: The amino acid sequence of protein BL10 from the 50S subunit of the *Bacillus* s
 A;Reference number: A02766
 A;Accession: A02766
 A;Molecule type: protein
 A;Residues: 1-177 <KIM>
 R;Ramakrishnan, V.; Gerchman, S.B.
 J. Biol. Chem. 266, 880-885, 1991
 A;Title: Cloning, sequencing, and overexpression of genes for ribosomal proteins from E
 C;Accession: B39085; MUID:91093267; PMID:1985969
 A;Accession: B39085
 A;Molecule type: protein
 A;Cross-references: GB:MS7622
 R;Uralaub, H.; Kraft, V.; Bischoff, O.; Mueller, B.C.; Wittmann-Liebold, B.
 EMBO J. 14, 4579-4588, 1995
 A;Title: Protein-rRNA binding features and their structural and functional implications
 A;Residues: 8-170 <DBM>
 A;Accession: S59051; MUID:96003638; PMID:7556101
 A;Molecule type: DNA
 A;Accession: S59061
 A;Cross-references: <URL>
 C;Superfamily: ribosomal protein L6/L9
 C;Keywords: protein biosynthesis; ribosome

Query Match Score 36; DB 2; Length 323;
 Best Local Similarity 70.0%; Pred. No. 18; Indels 2; Gaps 0;
 Matches 7; Conservative 1; Mismatches 2;
 Qy 1 TVSQNLTR 10
 Db 189 TVGENYLTVR 198

RESULT 3

B97534
 Biotin acid synthetase (lip-syn) (lipote synthase) [imported] - *Agrobacterium tumefaciens*
 C;Species: *Agrobacterium tumefaciens*
 C;Accession: B97534
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allingr, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*: A Reference Number: A97359; MUID:21608551; PMID:11743194
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-323 <KUR>
 A;Cross-references: GB:AE007869; PIDN:AAK81227.1; PID:g15156511; GSPDB:GN00169
 C;Genetics:
 A;Gene: AGR C 2646
 A;Map position: circular chromosome
 C;Superfamily: lipoic acid synthase

Query Match Score 36; DB 2; Length 323;
 Best Local Similarity 70.0%; Pred. No. 18; Indels 2; Gaps 0;
 Matches 7; Conservative 1; Mismatches 2;
 Qy 1 TVSQNLTR 10
 Db 189 TVGENYLTVR 198

RESULT 4

A89837
 hypothetical protein SA0619 [imported] - *Staphylococcus aureus* (strain N315)
 C;Species: *Staphylococcus aureus* (strain N315)
 C;Accession: A89837
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uti, Y.; Kobayashi, N.; Saikano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 LacZ 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
 A;Accession number: A89758; MUID:21311952; PMID:11418146
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-335 <KUR>
 A;Cross-references: GB:BA000018; PIDN:913700555; PIDN:BA841852.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: SA0619
 C;Superfamily: probable sodium-dependent phosphate transporter MTH1885
 Query Match Score 35; DB 2; Length 335;
 Best Local Similarity 70.0%; Pred. No. 29; Indels 2; Gaps 0;
 Matches 7; Conservative 1; Mismatches 2;
 Qy 1 TVSQNLTR 10
 Db 245 TVGENIMKIR 254

RESULT 5

R55S0F

Query Match Score 34; DB 2; Length 244;
 Best Local Similarity 75.0%; Pred. No. 33; Mismatches 0; Indels 0; Gaps 0;
 A;Introns: 12/2; 36/2
 C;Superfamily: conserved hypothetical protein YPR016C
 Query Match Score 34; DB 2; Length 244;
 Best Local Similarity 75.0%; Pred. No. 33; Mismatches 0; Indels 0; Gaps 0;
 A;Introns: 12/2; 36/2
 C;Genetics:
 A;Gene: SPDB:SPCC1919.09
 A;Map Position: 3
 A;Cross-references: <DN>
 A;Status: preliminary
 A;Molecule type: DNA
 A;Accessories: EMBL:AL035075; PIDN:CAA22640.1; GSPDB:GN000668; SPDB:SPCC1919.09
 A;Experimental source: strain 972h-; cosmid C1919
 C;Genetics:

RESULT 6

T41234
 translation initiation factor eIF-6 [imported] - fission yeast (Schizosaccharomyces pombe)
 C;Species: *Schizosaccharomyces pombe*
 C;Accession: T41234
 R;Lyne, M.; Harris, D.E.; Murphrey, L.D.; Rajandream, M.A.; Barrell, B.G., submitted to the EMBL Data Library, January 1999
 A;Reference number: Z21234
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Accession: T41234
 A;Cross-references: <DN>
 A;Residues: 1-244
 A;Experimental source: strain 972h-; cosmid C1919
 C;Genetics:

Query Match Score 34; DB 2; Length 244;
 Best Local Similarity 75.0%; Pred. No. 33; Mismatches 0; Indels 0; Gaps 0;
 A;Introns: 12/2; 36/2
 C;Superfamily: conserved hypothetical protein YPR016C
 Query Match Score 34; DB 2; Length 244;
 Best Local Similarity 75.0%; Pred. No. 33; Mismatches 0; Indels 0; Gaps 0;
 A;Introns: 12/2; 36/2
 C;Genetics:
 A;Gene: SPDB:SPCC1919.09
 A;Map Position: 3
 A;Cross-references: <DN>

RESULT 7

AB3218
 2-hydroxyacid dehydrogenase Atu5474 [imported] - *Agrobacterium tumefaciens* (strain C58,
 C;Species: *Agrobacterium tumefaciens*

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: AB3218
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2277; MUID:21608550; PMID:11741193
 A;Accession: AB3218
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-311 <KUR>
 A;Cross-references: GB:AB008687; PIDN:AAL4160..1; PMID:917743930; GSPDB:GN00188
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu5414
 A;Species: *Plasmid*
 C;Superfamily: phosphoglycerate dehydrogenase
 Query Match 72.3%; Score 34; DB 2; Length 311;
 Best Local Similarity 77.8%; Pred. No. 43;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 VSGNLTIR 10
 Db 288 VAGNLTYR 296

RESULT 8
 GB6335
 * hypothetical protein YreB [imported] - *Lactococcus lactis* subsp. *lactis* (strain III403)
 C;Species: *Lactococcus lactis* subsp. *lactis*
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 R;Boilotin, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissbach, J.; Ehr
 l; Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss
 A;Reference number: AB6625; MUID:21235186; PMID:11337171
 A;Accession: QB6635
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-314 <STO>
 A;Cross-references: GB:AB005176; PID:912724702; PIDN:AAK05785..1; GSPDB:GN00146
 A;Experimental source: strain III403
 C;Genetics:
 A;Gene: YreB

Query Match 72.3%; Score 34; DB 2; Length 314;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSGNLTIR 9
 Db 93 ISGNLTIR 100

RESULT 9
 A85939
 hypothetical protein Z4694 [imported] - *Escherichia coli* (strain O157:H7, substrate EDL9
 C;Species: *Escherichia coli*
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glassner, J.D.; Rose, D.J.; Mayne,
 iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: A85939
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1266 <STO>

A;Cross-references: GB:AE005174; NID:91217869; PIDN:AA58373..1; GSPDB:GN00145; UWGP:244
 A;Experimental source: strain O157:H7, substrate EDL933
 C;Genetics:
 A;Gene: Z4604
 C;Superfamily: *Escherichia coli* hypothetical protein yhdp
 Query Match 72.3%; Score 34; DB 2; Length 1266;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 TVSGNLTIR 9
 Db 1017 TISGNTLTL 1025

RESULT 10
 F91143
 hypothetical protein ECs4118 [imported] - *Escherichia coli* (strain O157:H7, substrate R:
 C;Species: *Escherichia coli*
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
 R;Accession: F91143
 R;Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gotoh, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno
 A;Reference number: A99629; MUID:21156231; PMID:1156231; PMID:11258796
 A;Accession: F91143
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1266 <STO>
 A;Cross-references: GB:BA0000007; PIDN:BA37541..1; PID:913363591; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrate RIMD 0509952
 C;Genetics:
 A;Gene: ECs4118
 C;Superfamily: *Escherichia coli* hypothetical protein yhdp
 Query Match 72.3%; Score 34; DB 2; Length 1266;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 TVSGNLTIR 9
 Db 1017 TISGNTLTL 1025

RESULT 11
 TPPII
 C;Species: Phage PI
 C;Accession: JS0460
 R;Guidolin, A.; Zingg, J.M.; Abber, W.
 Gene 76, 239-243, 1989
 A;Title: Organization of the bacteriophage PI tail-fibre operon.
 A;Reference number: PS0109; MUID:89326122; PMID:2526777
 A;Accession: JS0460
 A;Molecule type: DNA
 A;Residues: 1-144 <GTI>
 C;Genetics:
 C;Keywords: tail fiber protein R - phage PI
 A;Gene: R
 C;Superfamily: phage PI tail fiber protein R
 Query Match 70.2%; Score 33; DB 1; Length 144;
 Best Local Similarity 60.0%; Pred. No. 30;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 TVSGNLTIR 10
 Db 79 TYSGGTITR 88

RESULT 12

S16683 gene R protein - Escherichia coli plasmid p15B

C;Species: Escherichia coli

C;Accession: S16683

R;Sandmeier, H.; Iida, S.; Huebner, P.; Biestand-Nauer, R.; Arber, W.

Nucleic Acids Res. 19, 5831-5838, 1991

A;Title: Gene organization in the multiple DNA inversion region Min of Plasmid p15B of E

A;Reference number: S16680; MUID:92051368; PMID:1945872

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-144 <SAN>

A;Cross-references: ENBXL:X62121; NID:542224; PIDN:CA44046.1; PMID:942228

C;Genetics:

A;Gene: R

A;Genome: Plasmid

C;Superfamily: Phage PI tail fiber protein R

Query Match 70.2%; Score 33; DB 2; Length 144;

Best Local Similarity 60.0%; Pred. No. 30;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

Db 79 TVSGNLTIR 98

Qy 1 TVSGNLTIR 10

Db 79 TVSGNLTIR 98

A;Accession: B98106

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-426 <STO>

C;Species: Arabidopsis thaliana (mouse ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001

C;Accession: FB5253

R;Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 405, 769-771, 1999

A;Title: Sequence and analysis of chromosome 4 of the Plant Arabidopsis thaliana.

A;Reference number: A85001; PMID:20083488; PMID:10161798

A;Accession: FB5253

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-428 <STO>

C;Species: Arabidopsis thaliana hypothetical protein T12H17.50

C;Map Position: 4

C;Superfamily: Arabidopsis thaliana hypothetical protein T12H17.50

A;Accession: G95241

A;Title: Streptococcus pneumoniae (strain TIGR4)

A;Cross-references: GB:AE005672; PIDN:AAK76128.1; PMID:91497357; GSPDB:GN000164; TIGR:SP4

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP2065

Query Match 70.2%; Score 33; DB 2; Length 411;

Best Local Similarity 66.7%; Pred. No. 92;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 9

Db 30 SVAGNLTII 38

Qy 1 TVSGNLTIR 9

Db 30 SVAGNLTII 38

RESULT 14

B98106 hypothetical protein MATE transporter [imported] - Streptococcus pneumoniae (strain RG)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001

C;Accession: B98106

R;Boskina, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgert, S.; Dehoff, B.S.; E

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N

J.; Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain RG.

A;Reference number: A97872; MUID:21429245; PMID:11544234

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CM protein - protein search, using sw model

Run on: June 22, 2004, 08:41:07 ; Search time 7 Seconds
 (Without alignments) 74.386 Million cell updates/sec

Title: US-09-529-206D-4_COPY_127_136

Perfect score: 47

Sequence: 1 TYSGNLTIR 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Query Match Length DB ID Description

No.	Score	Query	Match	Length	DB	ID	Description
1	47	100.0	180	1	CTG1_HUMAN	P78358	homo sapien
2	38	80.9	322	1	LIP1_RHET	Q05941	rhizobium e
3	36	76.6	323	1	LIP1_AGRITS	Q8ufg1	agrobacteri
4	34	72.3	131	1	F1BA_PIG	Q77789	sus scrofa
5	34	72.3	177	1	RLE_EARST	P20291	bacillus st
6	34	72.3	244	1	IP6_SCROBO	Q94476	schizosacch
7	34	72.3	314	1	OR23_MOUSE	Q8vg09	mus musculu
8	34	72.3	314	1	OR28_MOUSE	Q8vg07	mus musculu
9	34	72.3	314	1	OR28_MOUSE	Q8vg04	mus musculu
10	34	72.3	314	1	OR32_MOUSE	Q8vf12	mus musculu
11	34	72.3	314	1	OR33_MOUSE	Q8vf11	mus musculu
12	34	72.3	314	1	OR34_MOUSE	Q8vf66	mus musculu
13	34	72.3	314	1	OR39_MOUSE	Q8vew5	mus musculu
14	34	72.3	314	1	OR40_MOUSE	Q8vgl3	mus musculu
15	34	72.3	316	1	OR22_MOUSE	Q8vf13	mus musculu
16	34	72.3	321	1	OR31_MOUSE	Q8vf13	mus musculu
17	34	72.3	323	1	OR29_MOUSE	Q8vg03	mus musculu
18	34	72.3	330	1	OR41_MOUSE	Q8vf12	mus musculu
19	34	72.3	330	1	OR42_MOUSE	P22946	bactericpha
20	33	70.2	144	1	VGR_BPP1	Q8xk11	clostridium
21	33	70.2	145	1	PHEB_CLOPE	Q9ng22	homo sapien
22	33	70.2	313	1	OPE2_HUMAN	Q9jw21	neisseria m
23	33	70.2	436	1	ARGA_NEIMA	Q9jxq9	neisseria m
24	33	70.2	436	1	ARGA_NEIMA	P50129	sus scrofa
25	33	70.2	470	1	SH2A_PIG	P18595	crictellus
26	33	70.2	471	1	SH2A_HUMAN	P28223	homo sapien
27	33	70.2	471	1	SH2A_MACMU	P50128	macaca mulatta
28	33	70.2	471	1	SH2A_MOUSE	P35363	mus musculu
29	33	70.2	471	1	SH2A_RAT	P14842	rattus norvegicus
30	33	70.2	471	1	CYAY_VIBPA	Q87k11	vibrio para
31	32	68.1	104	1	FABA_SPTR	P99p60	spermophilus
32	32	68.1	131	1	HIS2_PYRFU	P58853	pyrococcus
33	32	68.1	209	1			KW

ALIGNMENTS

34	32	68.1	245	1	IF6 YEAST
35	32	68.1	316	1	LY_BPSF6
36	32	68.1	323	1	O2AE_HUMAN
37	32	68.1	412	1	MTRL_HUMAN
38	32	68.1	418	1	SAHH_AQUAE
39	32	68.1	451	1	VS46_YEAST
40	32	68.1	455	1	VS11_REVOD
41	32	68.1	458	1	SH2C_HUMAN
42	32	68.1	459	1	SH2C_MOUSE
43	32	68.1	460	1	SH2C RAT
44	32	68.1	479	1	SH2B RAT
45	32	68.1	496	1	SYK_MYCA

RESULT¹

CTG1_HUMAN

STANDARD:

AC: P78358; PRT: 180 AA.

ID: CTG1_HUMAN

SEQUENCE FROM N.A.

MEDLINE=97201611; PubMed=9050879;

DT: 15-DEC-1998 (Rel. 37, Created)

DT: 15-DEC-1998 (Rel. 37, Last sequence update)

DT: 28-FEB-2003 (Rel. 41, Last annotation update)

DE: Cancer/testis antigen 1 (Autoimmunogenic cancer/testis antigen NY-ESO-1).

DS: 1).

RA: CTA1, OR CTAG.

OS: Homo sapiens (Human).

OC: Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;

NCBI_TaxID=9606;

RN: [1]

RP: SEQUENCE FROM N.A.

RC: TISSUE=Melanoma;

RX: MEDLINE=97289662; PubMed=9626360;

LA: Lethe B., Lucas S., Michaux L., Godelaine D., Serrano A.,

RA: de Plaein B., Boon T.,

PA: "A testicular antigen aberrantly expressed in human cancers detected by autologous antibody screening."

RT: Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).

RL: [2]

RP: SEQUENCE FROM N.A.

RC: TISSUE=Melanoma;

RX: MEDLINE=97289662; PubMed=9626360;

LA: Wang R.-P., Johnston S.L., Zeng G., Topalian S.L.,

RA: Schwartzentruber D.J., Rosenberg S.A.,

PA: "A breast and melanoma-shared tumor antigen: T cell responses to

RT: antigenic peptides translated from different open reading frames."

RL: J. Immunol. 161:3596-3606(1998).

RN: [3]

RP: SEQUENCE FROM N.A.

RC: MEDLINE=97430582; PubMed=9759882;

LA: Wang R.-P., Johnston S.L., Zeng G., Topalian S.L.,

RA: Schwartzentruber D.J., Rosenberg S.A.,

PA: "A breast and melanoma-shared tumor antigen: T cell responses to

RT: antigenic peptides translated from different open reading frames."

RL: J. Immunol. 161:3596-3606(1998).

CC: [-] TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide

CC: variety of cancers. Detected in uterine myometrium.

CC: [-] SIMILARITY: Belongs to the CTAG family.

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CC: between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC: the European Bioinformatics Institute. There are no restrictions on its

CC: use by non-profit institutions as long as its content is in no way

CC: modified and this statement is not removed. Usage by and for commercial

CC: entities requires a license agreement (See http://www.isb-sib.ch/announce/

CC: or send an email to license@isb-sib.ch).

CC: DR: EMBL; ISSN: 0309-0879; ISSN-L: 0309-0879; ISSN-2: 1471-8158;

DR: DR: ISSN: 0309-0879; ISSN-L: 0309-0879; ISSN-2: 1471-8158;

DR: ISSN: 0309-0879; ISSN-L: 0309-0879; ISSN-2: 1471-81

FT DOMAIN	5	82	GLY-RICH.
FT TRANSMEM	156	17992	POTENTIAL.
SEQ SEQUENCE	180 AA;	B122C5C2C8BE1569	CRC64;
Query Match	100.0%	Score 47; DB 1;	Length 180;
Best Local Similarity	100.0%	Pred. No. 0.024;	
Matches 10;	Conservative	Mismatches 0;	Indels 0;
Ov	1 TVSGNLTIR 10		Gaps
Dv	127 TVSGNLTIR 136		
RESULT 2			
LIPA_RHET	ID LIPA_RHET	STANDARD;	PRT; 322 AA.
AC 005941;	AC 005941;		
DD 15-JUL-1998	DD 15-JUL-1998 (Rel. 36, Created)		
DT 15-JUL-1998	DT 15-JUL-1998 (Rel. 36, Last sequence update)		
DE 28-FEB-2003	DE 28-FEB-2003 (Rel. 41, Last annotation update)		
GN Lipoic acid synthetase (Lip-syn) [lipoate synthase].			
OS Rhizobium etli.			
BB Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
NCBI_TAXID=39449;			
[1]			
RN			
RP			
SEQUENCE FROM N.A.			
STRAIN=CE3;			
RX MEDLINE=97286510; PubMed=9141657;			
Date R., Riccio A., Taccarino M., Patriarca E.J.-i			
RX Cloning and transcriptional analysis of the lipa (lipoic acid			
RX synthetase gene from Rhizobium etli.**			
RU PEMS Microbiol. Lett. 149:165-172 (1997).			
J- PUNCTION: Synthesis of alpha-(+)-lipoic acid. It may be involved			
J- in the sulfur insertion chemistry in lipoate biosynthesis (By			
J- similarity).			
CC -!- PATHWAY: Lipoate biosynthesis.			
CC -!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).			
CC -!- SIMILARITY: Belongs to the bictin and lipoic acid synthetases			
CC family.			
CC			
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CC tion between the Swiss Institute of Bioinformatics and the ENB outlet			
CC of the European Bioinformatics Institute. There are no restrictions on			
CC use by non-profit institutions as long as its content is in			
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CC cial entities requires a license agreement (See http://www.isb-sib.ch/)			
CC or send an email to license@isb-sib.ch).			
CC			
DR EMBL: Y11708; CAFA72400.1; -.			
DR HAMAP: MF_002016; -; 1.			
DR InterPro; IPR006638; EIP3.			
DR InterPro; IPR003638; Lipoate synth.			
DR InterPro; IPR007197; Radical_SAM.			
DR PF04035; Radical_SAM; 1.			
DR SMART; SM00729; EIP3; 1.			
DR TIGRFAPS; TIGR00510; lipoA; 1.			
KW LIPID-SULFUR.	87	IRON-SULFUR (POTENTIAL).	
FT METAL	91	IRON-SULFUR (POTENTIAL).	
FT METAL	94	IRON-SULFUR (POTENTIAL).	
SEQ SEQUENCE	322 AA;	36297 MW; 45E7.85214486847 CRC64;	
Query Match	1 TVSGNLTIR 10	Score 38; DB 1;	Length 322;
Best Local Similarity	70.0%	Pred. No. 3.1;	
Matches 7;	Conservative	Mismatches 2;	Indels 1;
Ov	1 TVSGNLTIR 10		Gaps
Dv	188 TVAGNYLTIVR 197		

Query Match Similarity	76.6%	Score	36	DB	1;	Length	323;	Pred. No.	8;	Best Local Matches	70.0%;	Mismatches	1;	Indels	2;	Gaps	0;	Best Local Similarity	60.0%;	Score	1	DB	1;	Length	8;	Pred. No.	8;
QY	1	TVSGNLTIR	10	DR	189	TVGNLYLTVR	198	DR	RL6_BACST	STANDARD;	PRT;	177 AA.															
RESULT 4				AC	PP2391;																						
FABP_PIG				ID	PP2391;																						
ID	O97788;	PIG		AC	O97788;	PIG																					
AC	097788;			ID	O97788;																						
DT	16-OCT-2001	(Rel.	40,	AC	097788;																						
DT	16-OCT-2001	(Rel.	40,	AC	097788;																						
DT	16-OCT-2003	(Rel.	42,	AC	097788;																						
DT	10-OCT-2003	(Rel.	42,	AC	097788;																						
DB	Fatty acid-binding protein, adipocyte (AFABP)			DB	505	Fatty acid-binding protein, adipocyte (AFABP)																					
DB	protein (ALBP) (AfABP) (Ap2).			GN	505	Fatty acid-binding protein, adipocyte (AFABP) (ALBP) (AfABP) (Ap2).																					
GN	FABP2.			GN	505	Fatty acid-binding protein, adipocyte (AFABP) (ALBP) (AfABP) (Ap2).																					
OS	Sus scrofa	(Fig).		OS	Sus scrofa	(Fig).																					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OC	Eukaryota; Metazoa; Chordata; Cetartiodactyla; Suina; Suidae; Sus.																						
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.																						
OX	NCBI_TaxID=9823;			OX	NCBI_TaxID=9823;																						
RN	[1]	-		RN	[1]	-																					
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.																						
RC	RC			RC	RC																						
RC	Daroc;	TISSUE=Liver;		RC	Daroc;	TISSUE=Liver;																					
RA	Gerbens P.N.A.; Jansen A.; van Bep A.J.M.; Harders F.;			RA	Gerbens P.N.A.; Jansen A.; van Bep A.J.M.; Harders F.;																						
RA	Meuwissen T.H.B.; Settemberger G.F.W.; Veerhamp J.H.; te Paas M.F.W.;			RA	Meuwissen T.H.B.; Settemberger G.F.W.; Veerhamp J.H.; te Paas M.F.W.;																						
RA	"The adipocyte fatty acid-binding protein locus: characterization and association with intramuscular fat content in pigs."			RA	"The adipocyte fatty acid-binding protein locus: characterization and association with intramuscular fat content in pigs."																						
RT	RT			RT	RT																						
RT	"The adipocyte fatty acid-binding protein locus: characterization and association with intramuscular fat content in pigs."			RT	"The adipocyte fatty acid-binding protein locus: characterization and association with intramuscular fat content in pigs."																						
RL	·.RL			RL	·.RL																						
RN	[2]	-		RN	[2]	-																					
RP	SEQUENCE OF 36-47, AND TISSUE SPECIFICITY.			RP	SEQUENCE OF 36-47, AND TISSUE SPECIFICITY.																						
RC	RC			RC	RC																						
RC	TISSUE=FAT;			RC	TISSUE=FAT;																						
RC	MEDLINE=90241113; PubMed=2334399;			RC	MEDLINE=90241113; PubMed=2334399;																						
RA	Armstrong M.K.; Berligh D.A.; Storch J.; Clarke S.D.;			RA	Armstrong M.K.; Berligh D.A.; Storch J.; Clarke S.D.;																						
RA	"The purification and characterization of a fatty acid binding protein specific to pig (Sus domesticus) adipose tissue,"			RA	"The purification and characterization of a fatty acid binding protein specific to pig (Sus domesticus) adipose tissue,"																						
RT	RT			RT	RT																						
RT	"Protein-RNA binding features and their structural and functional implications in ribosomes as determined by cross-linking studies."			RT	"Protein-RNA binding features and their structural and functional implications in ribosomes as determined by cross-linking studies."																						
RL	·.RL			RL	·.RL																						
CC	!- FUNCTION: Lipid transport protein in adipocytes. Binds both long chain fatty acid and retinoic acid. Involved in the regulation of subcutaneous fat accretion.			CC	!- FUNCTION: Lipid transport protein in adipocytes. Binds both long chain fatty acid and retinoic acid. Involved in the regulation of subcutaneous fat accretion.																						
CC	!- SUBCUTANEOUS LOCATION: Cytoplasmic (Potential).			CC	!- SUBCUTANEOUS LOCATION: Cytoplasmic (Potential).																						
CC	!- TISSUE SPECIFICITY: Adipose tissue.			CC	!- TISSUE SPECIFICITY: Adipose tissue.																						
CC	!- PTM: The N-terminus is blocked.			CC	!- PTM: The N-terminus is blocked.																						
CC	!- SIMILARITY: Belongs to the fatty-acid binding protein (FABP) family.			CC	!- SIMILARITY: Belongs to the fatty-acid binding protein (FABP) family.																						
CC	CC			CC	CC																						
CC	This SWISS-PROT entry is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			CC	This SWISS-PROT entry is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).																						
CC	EMBL; AJ16020; CAA79951;			CC	EMBL; AJ16020; CAA79951;																						
DR	HSSP; P01117; L1D			DR	InterPro; IPR000461; Fatty acid-BP																						
DR	InterPro; IPR000567; Lipocalin-CyteFABP.			DR	InterPro; IPR00061; Lipocalin; 1.																						
DR	Pfam; PF00061; Lipocalin; 1.			DR	PRINTS; PR000178; FATTYACIDBP.																						
DR	PRINTS; PR00178; FATTYACIDBP.			DR	PROSITE; PS0314; FABP; 1.																						
DR	PROSITE; PS0314; FABP; 1.			XW	Transport: Lipid-binding; phosphorylation.																						
XW	INIT MET	0		XW	INIT MET	0																					
FT	MOD_RES	19		FT	MOD_RES	19																					
FT	PHOSPHORYLATION (BY TYR KINASES)			FT	PHOSPHORYLATION (BY TYR KINASES)																						
SQ	SEQUENCE 131 AA;	14545 MW;	6566CB0CD4AB2 CRC64;	SQ	SEQUENCE 131 AA;	14545 MW;	6566CB0CD4AB2 CRC64;																				
Query Match	72.3%	Score	34;	DB	1;	Length	131;	FT	INIT_MET	0																	

olfactory receptor gene families.";
 RIL Hum. Mol. Genet. 11:535-546 (2002).
 RN [3]
 RP ERRATUM.
 RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
 RIL Hum. Mol. Genet. 11:1683-1683 (2002).
 CC -!!- FUNCTION: Potential odorant receptor.
 CC -!!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AY073356; AA616109; 1; -.
 DR InterPro; IPR01001; AAIP71001; 1; -.
 DR Pfam; PF00001; 7tm; 1.
 DR PRINTS; PR00237; GPIRRHODPSN.
 DR PROSITE; PS000237; G PROTEIN RECEPTOR_F1_1; 1.
 DR PROSITE; PS50952; G PROTEIN RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT TRANSMEM 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).
 FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 123 3 (POTENTIAL).
 FT DOMAIN 124 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 157 4 (POTENTIAL).
 FT DOMAIN 158 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 200 220 5 (POTENTIAL).
 FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 241 261 6 (POTENTIAL).
 FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 275 295 7 (POTENTIAL).
 FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 100 192 BY SIMILARITY.
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 314 AA; 34549 MW; E143B2A1E0321BD9 CRC64;

Query Match 72.3%; Score 34; DB 1; Length 314;
 Best Local Similarity 72.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLITI 9
 Db 41 TVSGNLSTI 49

RESULT 8
 OR25_MOUSE STANDARD; PRT; 314 AA.
 ID OR25_MOUSE STANDARD;
 AC Q8VG07;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Putative olfactory receptor 204-10.
 GN MOR204-10.
 OS Mus musculus (Mouse).
 OC Bivalvia; Mollusca; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10890;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=1678863; PubMed=11802173;
 RA Zhang X., Firestein S.;

"The olfactory receptor gene superfamily of the mouse.";
 RIL Nat. Neurosci. 5:124-133 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21864068; PubMed=11875048;
 RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
 Trask B.J.;
 RA RT Different evolutionary processes shaped the mouse and human
 olfactory receptor gene families.";
 RIL Hum. Mol. Genet. 11:535-546 (2002).
 RN [3]
 RP ERBATUM.
 RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
 Trask B.J.;
 RIL Hum. Mol. Genet. 11:1683-1683 (2002)
 CC -!!- FUNCTION: Potential odourant receptor.
 CC -!!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AY073358; AAL61021; 1; -.
 DR InterPro; IPR002716; GPCR_Rhodopsin.
 DR PRINTS; PR00237; GPCRHODOPSN.
 DR PROSITE; PS000237; G-PROTEIN RECEP_F1-1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEP_F1-2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 DR PRINTS; PR00237; GPCRHODOPSN.
 DR PROSITE; PS000237; G-PROTEIN RECEP_F1-1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEP_F1-2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).
 FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 123 3 (POTENTIAL).
 FT DOMAIN 124 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 157 4 (POTENTIAL).
 FT DOMAIN 158 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 200 220 5 (POTENTIAL).
 FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 241 261 6 (POTENTIAL).
 FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 275 295 7 (POTENTIAL).
 FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 100 192 BY SIMILARITY.
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 314 AA; 34658 MW; 71BC0839TC5884BD CRC64;

Query Match 72.3%; Score 34; DB 1; Length 314;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLITI 9
 Db 41 TVSGNLSTI 49

RESULT 9
 OR28_MOUSE STANDARD; PRT; 314 AA.
 ID OR28_MOUSE STANDARD;
 AC Q8VG04;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Putative olfactory receptor 204-13.
 GN MOR204-13.

Mus musculus (Mouse). Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus. NCBP_TAXID=10090; [1]

SEQUENCE FROM N.A. RXN MEDLINE:21864068; PubMed=11802173; RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L. RA Zhang X., Firestein S.; RT "The olfactory receptor gene superfamily of the mouse." ; RE Nat. Neurosci. 5:124-133 (2002). [2]

SEQUENCE FROM N.A. RXN MEDLINE:21864068; PubMed=11802173; RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L. RA Trask B.J.; RT "Different evolutionary processes shaped the mouse and human olfactory receptor gene families." ; RE Mol. Genet. 11:535-546 (2002). [3]

ERRATUM. RXN RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L. RA Trask B.J.; RE Hum. Mol. Genet. 11:1683-1683 (2002).

CC -!- FUNCTION: Potential odorant receptor.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors

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CC EMBL: AY073361; AAU16104.1; -.

DR AY17586; AAP10982.1; -.

DR InterPro: IPR0000276; GPCCR_Rhodopsin.

DR PFM: PP000001; 7tm_1..1.

DR PRINTS: PR00237; GPCR_RHODOPSN.

DR PROSITE: PS00237; G PROTEIN RECEP F1..1; 1.

DR PROSITE: PS50262; G PROTEIN RECEP F1..2; 1.

DR G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Olfaction.

FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 29 49 1 (POTENTIAL).

FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 58 78 2 (POTENTIAL).

FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 123 3 (POTENTIAL).

FT DOMAIN 124 136 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 137 157 4 (POTENTIAL).

FT DOMAIN 158 199 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 200 220 5 (POTENTIAL).

FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 241 261 6 (POTENTIAL).

FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 275 295 7 (POTENTIAL).

FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).

FT DISULFIDE 100 192 BY SIMILARITY.

FT CARBOXYD 8 8 N-LINKED (GLCNAC). (POTENTIAL).

ST SEQUENCE 314 AA: 34940 MW; 9761226104A6E7 CRC64;

SO

Query Match 72.3%; Score 34; DB 1; Length 314;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gap 0

QY 1 IVSGMILTI 9
DV 1 IVSGMILTI 49

Query Match Score 34 : DB 1; Length 314;
 Best Local Similarity Pred. No. 20;

RESUME

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

FT TRANSMEM 275 205 7 (POTENTIAL).
 FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 100 192 BY SIMILARITY.
 FT CARBOHYD 8 8 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC . .) (POTENTIAL).
 SQ SEQUENCE 314 AA; 34716 MW; 6DB1A4EB76BBC795 CRC64;

RESULT 11
 OR33_MOUSE STANDARD; PRT; 314 AA.
 OC Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Sciuromathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=11802173;
 RX MEDLINE=21676863; PubMed=11802173;
 RA Zhang X., Firestein S.;
 RA "The olfactory receptor gene superfamily of the mouse.";
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 5:124-133(2002).
 RN [2]
 RP SEQUENCE FROM N.A. PubMed=21676863; PubMed=11802173;
 RX MEDLINE=21676863; PubMed=11802173;
 RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L.,
 RA Trask B.J.;
 RA "Different evolutionary processes shaped the mouse and human
 olfactory receptor gene families";
 RA Hum. Mol. Genet. 11:535-546(2002).
 RN [3]
 RP ERATUM.
 RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L.,
 RA Trask B.J.;
 RL Hum. Mol. Genet. 11:1683-1683(2002).
 CC -!- FUNCTION: Potential odorant receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL: AY073600; AAL61263.1; -;
 DR AY317600; AAP70995.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR PF00001; 7tm_1;
 DR PRINTS: PRO0237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECV_P1_1;
 DR PROSITE: PS0262; G-PROTEIN_RECV_P1_2;
 RW G-Protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).
 FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 123 3 (POTENTIAL).
 FT DOMAIN 124 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 157 4 (POTENTIAL).
 FT DOMAIN 158 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 200 220 5 (POTENTIAL).
 FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 241 261 6 (POTENTIAL).
 FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
 DR IntePro: IPR00276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1;
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECV_P1_1;
 DR PROSITE: PS50262; G-PROTEIN_RECV_P1_2;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).

Query Match
Best Local Similarity 72.3%; Score 34; DB 1; Length 314;
Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVSGNLTI 9
Db 41 TVSGNLTI 49

RESULT 1.3

ID OR39_MOUSE STANDARD; PRT; 314 AA.

AC QAVENW6; DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB PURATIVE OLFACTORY RECEPTOR 204-34.
GN MOR204-34.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

* OC _TAXID=10090;

RN [1]

RP SEQUENCE FROM N.A.; MEDLINE=21678863; PubMed=11802173;

RX Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.; Zhang X., Firestein S.; "The olfactory receptor gene superfamily of the mouse." ; Nat. Neurosci. 5:124-133 (2002).

RN [2]

RP SEQUENCE FROM N.A.; MEDLINE=1861068; PubMed=11875048;

RX RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.; "Different evolutionary processes shaped the mouse and human olfactory receptor gene families"; Hum. Mol. Genet. 11:535-545 (2002).

RN [3]

RP BREATHUM. RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.; "FUNCTION: Potential odorant receptor."
RL Hum. Mol. Genet. 11:1683-1683 (2002).

CC "-!- FUNCTION: Potential odorant receptor."
CC "-!- SUBCELLULAR LOCATION: Integral membrane protein."
CC "-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors."

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CC DR PROSITE; PS00237; G-PROTEIN RECEP_P1_1; 1.
DR PROSITE; PS50265; G-PROTEIN_RBCBP_P1_2; 1.
KW G-Protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene Family; Olfaction.

DOMAIN 1 FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 29 49 1 (POTENTIAL).
FT TRANSMEM 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 78 2 (POTENTIAL).
FT TRANSMEM 79 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 123 3 (POTENTIAL).
FT TRANSMEM 124 136 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 137 157 4 (POTENTIAL).
FT TRANSMEM 158 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 220 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 221 240 5 (POTENTIAL).
FT TRANSMEM 241 261 6 (POTENTIAL).
FT TRANSMEM 262 274 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 275 295 7 (POTENTIAL).
FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).
DISULFID 100 192 BY SIMILARITY.
CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 314 AA; 34839 MW; P19098PAIE3D3C7D CRC64;

Query Match
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTI 9
Db 41 TVSGNLTI 49

RESULT 1.4

OR40_MOUSE STANDARD; PRT; 314 AA.

AC QAVENW5; DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB PURATIVE OLFACTORY RECEPTOR 204-35.
GN MOR204-35.

OS Mus musculus (Mouse).
OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

* OC _TAXID=10090;

RN [1]

RP SEQUENCE FROM N.A.; MEDLINE=21678863; PubMed=11802173;

RX RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.; "The olfactory receptor gene superfamily of the mouse." ; Nat. Neurosci. 5:124-133 (2002).

RN [2]

RP SEQUENCE FROM N.A.; MEDLINE=21864056; PubMed=11875048;

RX RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.; "FUNCTION: Potential odorant receptor."
RA Trask B.J.; "DIFFERENT EVOLUTIONARY PROCESSES SHAPED THE MOUSE AND HUMAN OLFACTORY RECEPTOR GENE FAMILIES"; Nat. Mol. Genet. 11:535-545 (2002).

RN [3]

RP ERRATUM. RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.; "FUNCTION: Potential odorant receptor."
RL Hum. Mol. Genet. 11:1683-1683 (2002).

CC "-!- FUNCTION: Potential odorant receptor."
CC "-!- SUBCELLULAR LOCATION: Integral membrane protein."
CC "-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors."

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CC DR EMBL; A1073782; AAL61445; 1.
CC DR EMBL; A1317618; AAF71008; 1.
CC DR InterPro; IPR000276; GICR_Rhodopsin.
PFam; PF00001; 7tm_1; 1.
CC DR PRINTS; PRO0237; GPCR_RHODOPSIN.

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CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC	EMBL: AY07783; AAH61446; 1;
DR	EMBL: AY317601; AAP70996; 1;
DR	InterPro: IPR000275; GPCR_Rhodopsin.
DR	Pfam: PF00061; 7tm; 1..1.
DR	PRINTS: PRO0237; GPCR_RHODOPSIN.
DR	PROSITE: PS00237; G-PROTEIN_RECESP_P1_1; 1..1.
DR	PROSITE: PS00237; G-PROTEIN_RECESP_P1_2; 1..1.
DR	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Multigene family; Olfaction.
DOMAIN	1 28 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 29 49 1 (POTENTIAL).
FT	TRANSMEM 50 57 2 (POTENTIAL).
FT	TRANSMEM 58 78 3 (POTENTIAL).
FT	TRANSMEM 79 102 4 (POTENTIAL).
FT	TRANSMEM 103 123 5 (POTENTIAL).
FT	TRANSMEM 124 136 6 (POTENTIAL).
FT	TRANSMEM 137 157 7 (POTENTIAL).
FT	TRANSMEM 158 199 8 (POTENTIAL).
FT	TRANSMEM 200 220 9 (POTENTIAL).
FT	TRANSMEM 221 240 10 (POTENTIAL).
FT	TRANSMEM 241 261 11 (POTENTIAL).
FT	TRANSMEM 262 274 12 (POTENTIAL).
FT	TRANSMEM 275 295 13 (POTENTIAL).
FT	TRANSMEM 296 314 14 (POTENTIAL).
FT	DISULFID 100 192 BY SIMILARITY.
CARBOND	8 34953 MW: 99D8516B39F6B54D CRC64;
SEQUENCE	314 AA: 34953 MW: 99D8516B39F6B54D CRC64;
Query Match	Best Local Similarity 72.3%; Score 34; DB 1; Length 314;
Matches	7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy	1 TVSGNLITI 9
Db	41 TVSGNLITI 49
Result 15	Score 34; DB 1; Length 316;
OR22_MOUSE	ID OR22_MOUSE STANDARD; PRT; 316 AA.
AC	Q8VG13;
DT	10-OCT-2003 (Rel. 42, Created)
DT	10-OCT-2003 (Rel. 42, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Putative olfactory receptor 204-7.
GN	MOR204-7.
OS	Mus musculus (Mouse).
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Eukaryota; Metazoia; Chordata; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID:10090;
RN	[1]
RP	SEQUENCE FROM N.A. MEDLINE=21864068; PubMed=11802173;
RX	Young J.M., Friedmann C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.; "The olfactory receptor gene superfamily of the mouse." ; Nat. Neurosci. 5:124-133 (2002).
RN	[2]
RP	SEQUENCE FROM N.A. MEDLINE=21864068; PubMed=11875048; Young J.M., Friedmann C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.; "Different evolutionary processes shaped the mouse and human olfactory receptor gene families." ; Hum. Mol. Genet. 11:535-546 (2002).
RN	[3]
RP	ERRATUM. Young J.M., Friedmann C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.; "The olfactory receptor gene superfamily of the mouse." ; Nat. Neurosci. 5:124-133 (2002).
RX	-!- FUNCTION: Potential odorant receptor.

Query	TVSGNLITI	1	Best Local Similarity	72.3%
Matches	7; Conservative	1; Mismatches	1; Indels	0; Gaps 0;
Qy	TVSGNLITI	9	Db	TVSGNLITI 49
Search completed:	June 22, 2004,	Job time :	8 secs	

GN LAGE1.	AC 064327;	DT 01-AUG-1998 (TREMBLrel. 07; Created)
OS Homo sapiens (Human).	DT 01-AUG-1998 (TREMBLrel. 07; Last sequence update)	
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)	
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo;	DE GPB13.	
OX NCBI_TaxID=9606;	GN GENB_13.	
RN [1]	OS Bacteriophage N15.	
RP SEQUENCE FROM N.A.	OC Viruses; dsDNA viruses, no RNA stage; Caudovirales: Siphoviridae;	
TISSUE=Meջanoma;	OC Lambda-like viruses.	
RX MEDLINE=93325550; PubMed=10399963;	OX NCBI_TaxID=40631;	
RA Arnoultse C.A., Van den Doe! P.B., Heemskerk B., Schrier P.I.;	RN RP SEQUENCE FROM N.A.	
RT "unexpected t-cell-induced, melanoma-specific T cells recognize CMEL, an	RA Hendrix R.W., Ravin V.K., Casjens S.R., Ford M.E., Ravin N.V.,	
RL Int. J. Cancer 82:442-448(1999).	RA Smirnov I.K.;	
RP SEQUENCE FROM N.A.	RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.	
RA Aradhyu S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,	DR EMBL: AF064539; AAC19050.1; -.	
RA Patran H., Ciccodicola A., Kenrick S., Platzer M., D'Urso M.,	DR PIR: T13099; T13099.	
RA Nelson D.L.;	DR InterPro: IPR03343; Big_2.	
RT "multiple pathogenic and benign genomic rearrangements occur at a 35-	DR InterPro: IPR039364; Invasion_intimin.	
kb duplication involving the NEMO and the LAGE2 genes.";	DR PFAM: PF02368; Big_2.1.	
RL Hum. Mol. Genet. 0:0-0(2001).	DR SMART: SM00635; BID_1; 1.	
DR EMBL: AF277315; CAI10194.1; -.	DR SEQUENCE: 245 AA; 25571 MW; 2CC941997C103FD3 CRC64;	
SQ SEQUENCE 180 AA; 18236 MW; 9077FAP953543A25 CRC64;	Query Match Score 76.6%; Score 36; DB 9; Length 245;	
Query Match Best Local Similarity 77.8%; Pred. No. 40; Indels 0; Gaps 0;	Best Local Similarity 77.8%; Pred. No. 40; Indels 0; Gaps 0;	
Best Local Similarity 80.9%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;	Qy 1 TVSGNLT 9	
Best Local Similarity 80.0%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;	Db 209 TVSGNLTV 217	
Qy 1 TVSGNLT 10	RESULT 5	
Db 127 TVSGNLLFIR 136	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	ID Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	AC Q8EAQ4;	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	AC Q8EAQ4;	PRELIMINARY; PRT: 318 AA.
RA Read T.D., Eisen J.A., Seshadri R., Ward R.A., Clayton R.A.,	AC Q8EAQ4;	PRELIMINARY; PRT: 318 AA.
RA Meyer T., Tsapin A., Scott J., Beaman M., Methé B., Daugherty S.,	AC Q8EAQ4;	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	AC Q8EAQ4;	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	AC Q8EAQ4;	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	AC Q8EAQ4;	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	AC Q8EAQ4;	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	AC Q8EAQ4;	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	AC Q8EAQ4;	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .	
OS <i>Bifidobacterium longum</i> .	OC Bacteria: Proteobacteria: Alteromonadales:	
OC <i>Bifidobacteriaceae</i> ; <i>Shewanellia</i> .	OC Alteromonadaceae; <i>Shewanellia</i> .	
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RN STRAIN=NPR-1;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Read T.D., Eisen J.A., Seshadri R., Ward R.A., Clayton R.A.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Meyer T., Tsapin A., Scott J., Beaman M., Methé B., Daugherty S.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .;	
OS <i>Bifidobacterium longum</i> .	OC Biotechnol. 20:118-1123 (2002).	
OC <i>Bifidobacteriaceae</i> ; <i>Bifidobacterium</i> .	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RC STRAIN=NCC 2705;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22294977; PubMed=12381787;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Scheifele M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .;	
OS <i>Bifidobacterium longum</i> .	OC Biotechnol. 20:118-1123 (2002).	
OC <i>Bifidobacteriaceae</i> ; <i>Bifidobacterium</i> .	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RN STRAIN=NPR-1;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Read T.D., Eisen J.A., Seshadri R., Ward R.A., Clayton R.A.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Meyer T., Tsapin A., Scott J., Beaman M., Methé B., Daugherty S.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .;	
OS <i>Bifidobacterium longum</i> .	OC Biotechnol. 20:118-1123 (2002).	
OC <i>Bifidobacteriaceae</i> ; <i>Bifidobacterium</i> .	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RN STRAIN=NPR-1;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Read T.D., Eisen J.A., Seshadri R., Ward R.A., Clayton R.A.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Meyer T., Tsapin A., Scott J., Beaman M., Methé B., Daugherty S.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .;	
OS <i>Bifidobacterium longum</i> .	OC Biotechnol. 20:118-1123 (2002).	
OC <i>Bifidobacteriaceae</i> ; <i>Bifidobacterium</i> .	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RN STRAIN=NPR-1;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Read T.D., Eisen J.A., Seshadri R., Ward R.A., Clayton R.A.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Meyer T., Tsapin A., Scott J., Beaman M., Methé B., Daugherty S.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .;	
OS <i>Bifidobacterium longum</i> .	OC Biotechnol. 20:118-1123 (2002).	
OC <i>Bifidobacteriaceae</i> ; <i>Bifidobacterium</i> .	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RN STRAIN=NPR-1;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Read T.D., Eisen J.A., Seshadri R., Ward R.A., Clayton R.A.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Meyer T., Tsapin A., Scott J., Beaman M., Methé B., Daugherty S.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .;	
OS <i>Bifidobacterium longum</i> .	OC Biotechnol. 20:118-1123 (2002).	
OC <i>Bifidobacteriaceae</i> ; <i>Bifidobacterium</i> .	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RN STRAIN=NPR-1;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Read T.D., Eisen J.A., Seshadri R., Ward R.A., Clayton R.A.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Meyer T., Tsapin A., Scott J., Beaman M., Methé B., Daugherty S.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .;	
OS <i>Bifidobacterium longum</i> .	OC Biotechnol. 20:118-1123 (2002).	
OC <i>Bifidobacteriaceae</i> ; <i>Bifidobacterium</i> .	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RN STRAIN=NPR-1;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Read T.D., Eisen J.A., Seshadri R., Ward R.A., Clayton R.A.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Meyer T., Tsapin A., Scott J., Beaman M., Methé B., Daugherty S.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .;	
OS <i>Bifidobacterium longum</i> .	OC Biotechnol. 20:118-1123 (2002).	
OC <i>Bifidobacteriaceae</i> ; <i>Bifidobacterium</i> .	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RN STRAIN=NPR-1;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Read T.D., Eisen J.A., Seshadri R., Ward R.A., Clayton R.A.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Meyer T., Tsapin A., Scott J., Beaman M., Methé B., Daugherty S.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .;	
OS <i>Bifidobacterium longum</i> .	OC Biotechnol. 20:118-1123 (2002).	
OC <i>Bifidobacteriaceae</i> ; <i>Bifidobacterium</i> .	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RN STRAIN=NPR-1;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Read T.D., Eisen J.A., Seshadri R., Ward R.A., Clayton R.A.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Meyer T., Tsapin A., Scott J., Beaman M., Methé B., Daugherty S.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Pridmore R.D., Arigoni P.; Desiere F., Bork P., Delley M.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RT "The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
DB Possible cobyrinic acid synthase CobQ.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
GN BL0429.	OS <i>Shewanella oneidensis</i> .;	
OS <i>Bifidobacterium longum</i> .	OC Biotechnol. 20:118-1123 (2002).	
OC <i>Bifidobacteriaceae</i> ; <i>Bifidobacterium</i> .	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
OX NCBI_TaxID=216816;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RP SEQUENCE FROM N.A.	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RN STRAIN=NPR-1;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RX MEDLINE=22237686; PubMed=12368813;	Q8EAQ4	PRELIMINARY; PRT: 318 AA.
RA Heidelberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,	Q8EAQ4	PRELIMINARY; PRT: 318 AA.

RESULT 6

Q9HY4	PRELIMINARY;	PRT;	352 AA.	
AC	O9HY4;			
DT	01-MAY-1999 (TREMBREL 10; Created)			
DT	01-JUN-2003 (TREMBREL 24; Last sequence update)			
DE	Putative odorant receptor LQR1.			
OS	Lampetra fluviatilis (River Lamprey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;			
OC	Petromyzontiformes; Petromyzontidae; Lampetra.			
OX	NCBI_TaxID=7748;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Olfactory organ;			
RA	Berghard A., Dryer D.;			
RL	J. Neurobiol. 0:0 (01/1998).			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
DR	-!- SIMILARITY: BELONGS TO MEMBRANE 1 OF G-PROTEIN COUPLED RECEPTORS.			
EMBL	AF069546; AAC82381.1; -			
DR	GO:0016221; C: integral to membrane; IBA.			
DR	GO: GO:0014872; F: receptor activity; IBA.			
DR	GO: GO:001584; F: rhodopsin-like receptor protein signalin. . . IEA.			
DR	GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.			
DR	InterPro; IPR00276; GPCR_Rhodpsn.			
DR	PFAM; PF00001; 7tm 1; 1.			
PRINTS	PR00237; GPERRHODOPSN			
DR	PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1; 1.			
DR	PROSITE; PS50282; G PROTEIN RECEPTOR_F1_2; 1.			
XW	G-protein coupled receptor; Receptor_Transmembrane.			
SEQUENCE	352 AA; 40276 MW; 6366743DFFA9P4B CRC64;			
* SQ				
Query Match	76.6%;	Score 36;	DB 13;	Length 352;
Best Local Similarity	88.9%;	Pred No.	58;	
Matches	8;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
Qy	1 TVSGNLTI 9			
Db	45 TVVGNLTI 53			
RESULT 7				
Q9R391	PRELIMINARY;	PRT;	450 AA.	
AC	Q9R391;			
DT	01-MAY-2000 (TREMBREL 13; Created)			
DT	01-MAY-2000 (TREMBREL 13; Last sequence update)			
DT	01-OCT-2003 (TREMBREL 25; Last annotation update)			
DB	Secreted endo-1,4-beta-xylanase (EC 3.2.1.8).			
GN	XYSA OR SCO0674 OR SCP91_34C			
OS	Streptomyces coelicolor.			
OC	Bacteria; Actinobacteria; Actinomycetales;			
OC	Streptomycetaceae; Streptomyces; Streptomyces			
NCBI_TaxID=1902;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=A3 (2);			
RA	Oliver K., Harris D.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=A3 (2); MBDLINE=9700051; PubMed=844346;			
RX	Redenbach M., Kieser H.M., Denapaité D., Eichner A., Culum J., Kinashi E., Hopwood D.A.;			
RA	"A set of ordered cosmids and a detailed genetic and physical map for			
RT	the 8 Mb Streptomyces coelicolor A3 (2) chromosome.";			
RL	PL Mol. Microbiol. 21:77-96 (1996)."			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=A3 (2) / MI 45;			
RX	MEDLINE=21993410; PubMed=12000953;			
RA	Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Hiddle J.J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S., Rabinowitzsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Taylor K., Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.;"			
RA	"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3 (2)";			
RT	Nature 417:141-147 (2002).			
RL	EMBL; AL939106; CAB61191.1; -			
CC	HSSP; P07986; 1EXP.			
DR	GO: GO:0004553; F: hydrolase activity, hydrolyzing O-glycosyl . . . IEA.			
DR	GO: GO:0005975; P: carbohydrate metabolism; IBA.			
DR	InterPro; IPR01919; Baculo-bind.			
DR	InterPro; IPR008965; Cellulose-bind.			
DR	InterPro; IPR00000; Glyco_Hydro_10.			
DR	Pfam; PF00553; CEM 2, 1.			
DR	PRINTS; PR0033_L1; Glyco_hydro_10; 1.			
DR	SMART; SM00537; CBD_II_1.			
DR	SM00613; Glyco_001.			
DR	PROSITE; PS00591; GLYCOSIDASE_HYDROL_F10; 1.			
KW	Glycosidase; Hydrolase; X_Fan degradation; Complete proteome.			
SQ	SEQUENCE 450 AA; 41090 MW; B2PF6A36EC29B6AE CRC64;			
Query Match	76.6%;	Score 36;	DB 16;	Length 450;
Best Local Similarity	60.0%;	Pred No. 75;		
Matches	6;	Conservative	3;	Mismatches 1; Indels 0; Gaps 0;
Qy	1 TVSGNLTIR 10			
Db	405 TVSGNVATVR 414			
RESULT 8				
Q9R398	PRELIMINARY;	PRT;	36 AA.	
ID	Q9R398			
AC	Q9R398;			
RC	PRELIMINARY;			
RA	Q9R398; PRELIMINARY;			
RL	AC Q9R398;			
CC	DT DT 01-JUN-2003 (TRIMBLrel. 24; Created)			
DR	DT DT 01-JUN-2003 (TRIMBLrel. 24; Last sequence update)			
DR	DT DT 01-OCT-2003 (TRIMBLrel. 24; Last annotation update)			
DB	DE Lipoprotein, function unknown.			
GN	BN0817.			
OS	OS Bacteroides thetaiotaomicron.			
OC	OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales; Bacteroidaceae; Bacteroides.			
NCBI_TaxID=1918;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=A3 (2);			
RA	Oliver K., Harris D.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=A3 (2); MBDLINE=9700051; PubMed=844346;			
RX	Redenbach M., Kieser H.M., Denapaité D., Eichner A., Culum J., Kinashi E., Hopwood D.A.;			
RA	"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";			
RT	Science 299:2074-2076 (2003).			
RL	EMBL; AB016329; AA07524; 1.			
DR	InterPro; IPR002298; NIPB InterPro; IPR000437; Prok_lipoprot_S.			
DR	Pfam; PF04170; NIPB; 1.			
DR	PROSITE; PS00013; PROKAR_LIPOPOTINE; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 144 AA; 15781 MW; AB28358876E697B CRC64;			
Query Match	74.5%;	Score 35;	DB 16;	Length 144;

RA Zheng X.H.; Zhong F.N.; Zhong W.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.,
RA Gibbs R.A.; Myers E.W.; Rubin G.M.; Venter J.C.; "The genome sequence of Drosophila melanogaster";
RT Science 287:2185-2195 (2000);
RL 3MBL; AB013560; AAF50630.1;
DR FlyBase; FBgn0035724; CG10064.
DR InterPro; IPR001680; WD40.
DR Pfam; PF04400; WD40; 10.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00320; WD40; 8.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 4.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 742 AA; 81994 MW; B6F3210064859141 CRC64;

Query Match 74.5%; Score 35; DB 5; Length 742;
Best Local Similarity 66.7%; Pred. No. 2.1e+02; Length 742;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSGNLTIR 10
Db 154 ISGNALTVR 162

RESULT 15

Q8T4D0 PRELIMINARY; PRT; 742 AA.
ID Q8T4D0
AC
DT 01-JUN-2002 (TREMBLrel. 21; Created)
DT 01-JUN-2002 (TREMBrel. 21; Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24; Last annotation update)
DE AT03371P.
GN CG10064.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
* OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
EPHYDIOidea; Drosophilidae; Drosophila.
OX NCBI_TaxID:7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M.; Brookstein P.; Hong L.; Agbayani A.; Carlson J.;
RA Chame M.; Chavez C.; Dorsett V.; Drezenek D.; Frise E.,
RA George R.; Gonzalez M.; Guarini H.; Kronmiller B.; Li P.; Liao G.,
RA Miranda A.; Mungall C.J.; Nunoco J.; Paragis V.; Park S.,
RA Patel S.; Phouanenavong S.; Wan K.; Yu C.; Lewis S.E.; Rubin G.M.,
RA Celiker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY059248; AALd9986.1; CG10064.
DR FlyBase; FBgn0035724; CG10064.
DR InterPro; IPR001680; WD40.
DR Pfam; PF04400; WD40; 10.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00320; WD40; 10.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 4.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 742 AA; 82012 MW; BC13210535849140 CRC64;
Query Match 74.5%; Score 35; DB 5; Length 742;
Best Local Similarity 66.7%; Pred. No. 2.1e+02; Length 742;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSGNLTIR 10
Db 154 ISGNALTVR 162

Search completed: June 22, 2004, 08:53:26
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:40:22 ; Search time 68.6667 Seconds

(without alignments)

82.295 Million cell updates/sec

Title: US-09-529-206D-4_COPY_43_62

Perfect score: 107

Sequence: 1 RGERGAGARASPGGGAPR 20

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched:

1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04;*
 1: GeneseqP1980s;*
 2: GeneseqP1990s;*
 3: GeneseqP2000s;*
 4: GeneseqP2001s;*
 5: GeneseqP2002s;*
 6: GeneseqP2003as;*
 7: GeneseqP2003bs;*
 8: GeneseqP2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	107	100.0	20	2	AAY05979		Aay05979 Human can
2	107	100.0	180	2	AAYW62584		Aaw62584 Cancer, as
3	107	100.0	180	2	AAYW69665		Aaw69665 Human NY-
4	107	100.0	180	2	AAY05965		Aay05965 Human can
5	107	100.0	180	3	AAY52430		Aay52430 Human tum
6	107	100.0	180	3	AAY70862		Aay70862 Human tum
7	107	100.0	180	3	AAB03154		Aab03154 Human oes
8	107	100.0	180	4	AAB69946		Aab69946 Human NY-
9	107	100.0	180	4	AAG67164		Aag67164 Amino aci
10	107	100.0	180	4	AAU01535		Aau01535 Human NY-
11	107	100.0	180	4	AAE07714		Aae07714 Human NY
12	107	100.0	180	5	AAB84818		Aab84818 Human NYN
13	107	100.0	180	5	AAU1543		Aau1543 Human tum
14	107	100.0	180	6	AAB58672		Abr58672 Human can
15	107	100.0	180	6	ABR48210		Abr48210 Human bla
16	107	100.0	180	6	ABU56508		Abu56508 Lung canc
17	107	100.0	180	6	ABU56694		Abu56694 Lung canc
18	107	100.0	180	6	ABP74198		Abp74198 Human NY-
19	107	100.0	180	6	ABR84338		Abr84338 Human NY-
20	107	100.0	180	7	ADC09577		Adc09577 NY-ESO-1
21	107	100.0	180	7	ADD35568		Add35568 Human NY-
22	107	100.0	180	7	ADD25510		Add25510 Binding d
23	107	100.0	397	4	AAC13122		Aac13122 NY-ESO-IC
24	102	95.3	30	5	AAU85105		Aau85105 Human NYN
25	102	95.3	3541	5	AAU85130		Aau85130 Human NYN

ALIGNMENTS

RESULT 1
 ID AAY05979 standard; peptide; 20 AA.

XX
 AC AAY05979;
 XX DT 16-AUG-1999 {First entry}
 XX DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
 XX
 NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; thymoma; colon cancer;
 KW metastasis; melanoma; adenocarcinoma; uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; immunotherapy; therapy;
 KW vaccine.

XX Homo sapiens.

OS Synthetic.
 OS
 XX
 PR WO9918206-A2.

XX PD 15-APR-1999.
 XX PF 21-SEP-1998;

XX PR 08-OCT-1997;
 XX PR 08-OCT-1997 & 97HS-0061428P.
 XX PR (US DEPT HEALTH & HUMAN SERVICES .

PA PA (US DEPT HEALTH & HUMAN SERVICES .
 XX PA Wang RF, Rosenberg SA;

XX DR WPI; 1999-277270/23.

XX PT Cancer antigen NY ESO1/CAG-3 .

XX PS Claim 16; Page 64; 88pp; English.

XX
 CC The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precursor; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide

or tumour antigen; antibodies reacting with a CRG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a patient.

Sequence 20 AA;

Query Match 100.0%; Score 107; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.3e-06; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 RGPRGAGAARASPGGGAPR 20
Db 1 RGPRGAGAARASPGGGAPR 20

Sequence 180 AA;

Query Match 100.0%; Score 107; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.6e-05; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 SGRPRGAGAARASPGGGAPR 20
Db 43 RGRGRGAGAARASPGGGAPR 62

RESULT 2
AAW62584 Standard; protein; 180 AA.

ID AAW62584 Standard; protein; 180 AA.
XX AAW62584;
AC AAW62584;

XX 17-SEP-1998 (First entry)

DE Cancer associated antigen NY-ESO-1.

XX Cancer associated antigen; NY-ESO-1; regression; progression; onset; cancer; treatment; diagnosis.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Misc-difference 7 /note= "potential myristylation site"

FT Misc-difference 9 /note= "potential myristylation site"

FT Misc-difference 11 /note= "potential phosphorylation site"

FT Misc-difference 98 /note= "potential phosphorylation site"

FT Misc-difference 134 /note= "potential phosphorylation site"

FT Misc-difference 138 /note= "potential phosphorylation site"

XX PN WO9814464 A1.

XX PD 09-APR-1998.

XX PP 15-SEP-1997; 97WO-US016335.

XX PR 03-OCT-1996; 96US-00725182.

PA (LUDWIG INST CANCER RBS.

XX PI Chen Y, Scanlan M, Gure A, Old LJ, Jager B, Knuth A;

PI Drijfhout JW;

XX DR 1998-286417/25.

DR N-PSDB; AAV38566.

XX PT New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.

XX PS Claim 8; Fig 3; 49PP; English.

XX CC The present sequence represents a cancer associated antigen. The clone

CC from which the DNA sequence is obtained is designated NY-ESO-1. The CC specification describes a method for determining regression, progression CC of onset of a cancerous condition, comprising monitoring a sample from a CC patient with the cancerous condition for a parameter selected from NY-ESO CC -1 protein, a peptide derived from NY-ESO-1 protein and cytoytic T cells CC specific for the peptide and an HLA molecule with which it non-covalently CC complexes. Methods for the treatment of a cancerous condition are also CC described. The NY-ESO-1 protein and peptides derived from it can be used CC for diagnosis and treatment of cancers and to monitor the efficacy of a CC therapeutic regime

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.6e-05; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 SGRPRGAGAARASPGGGAPR 20
Db 43 RGRGRGAGAARASPGGGAPR 62

RESULT 3
AAW69665 Standard; protein; 180 AA.

ID AAW69665 Standard; protein; 180 AA.

XX AAW69665;

AC AAW69665;

XX DT 27-OCT-1998 (first entry)

DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.

XX DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.

XX Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

XX Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

XX Homo sapiens.

OS WO9832055-A1.

XX PN WO9832055-A1.

XX DD 30-JUL-1998.

XX PP 27-JAN-1998; 98WO-US001445.

XX PR 27-JAN-1997; 97US-00791495.

XX PA (LUDWIG INST CANCER RES.

XX PI Lethe B, Lucas S, De Smet C, Godellaire D, Boon-Falleur T;

XX XX DR 1998-427951/36.

XX DR N-PSDB; AAV50348.

XX PT New isolated LAGE-1 tumour associated nucleic acids - used to develop

PT products for the diagnosis and treatment of LAGE-1 associated disorders.

XX XX PT particularly tumours.

XX XX PS Example 2; Page 57-58; 73PP; English.

XX CC The present sequence represents human NY-ESO-1, formerly known as LL-1.2 CC clone, which is used in an example from the present invention which CC describes LAGE-1 tumour associated protein (TAP). The present invention CC also describes: (1) a method for treating a subject with a disorder CC characterised by expression of a LAGE-1 nucleic acid molecule or an CC expression product, comprising administering to the subject the disorder, where the cytolytic T cells to ameliorate the disorder, where the cytolytic T cells CC are specific for complexes of an HLA molecule and a LAGE-1 TAP or an CC immunogenic fragment; (2) a method for treating a subject with a disorder CC characterised by expression of a LAGE-1 nucleic acid molecule or an CC expression product, comprising administering a LAGE-1 TAP or an CC immunogenic fragment to ameliorate the disorder; and (3) a method for CC selectively enriching a population of T cells with cytolytic T cells CC specific for a LAGE-1 TAP comprising contacting an isolated population of CC T cells with an agent presenting a complex of a LAGE TAP or an CC immunogenic fragment and a HLA presenting molecule to selectively enrich

CC the isolated population of T cells with the cytolytic T cells. The
 CC methods and products from the present invention can be used for the
 CC diagnosis and treatment of LAGE-1 associated disorders, particularly
 CC tumours

XX Sequence 180 AA;

Query Match Score 100.0%; Score 107; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAAARASGPGGAPR 20
 Db 43 RGPRGAAARASGPGGAPR 62

RESULT 4
 AAY05965 standard; protein; 180 AA.

XX
 AC AAY05965;
 XX DT 16-AUG-1999 (first entry)
 DE Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
 XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
 KW melanoma; adenocarcinoma; Hodgkin's lymphoma; lung cancer; metastasis;
 KW non-Hodgkin's lymphoma; Hodgkin's lymphoma; colon cancer; uterine cancer;
 KW breast cancer; prostate cancer; ovarian cancer; cervical cancer;
 KW bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;
 KW tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
 XX Homo sapiens.
 XX OS WO9918206-A2.
 PD 15-APR-1999.
 XX PF 21-SEP-1998; 98W0-US019609.
 XX PR 08-OCT-1997; 97US-0061428P.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Wang RF, Rosenberg SA;
 XX DR 1999-2772270/23.
 DR N-PSD1; A0X58599.
 XX Cancer antigen NY ESO1/CAG-3.

XX Claim 4; Fig 3A; 89pp; English.

XX The present sequence represents the ORF1 protein encoded by open reading
 frame 3 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and
 potent tumour antigen capable of eliciting an antigen specific immune
 response by T cells. Cancer peptides comprising ORF1, ORP2 (see
 AAY05966), portions of these peptides and their variants (see AAY05965-
 87), are useful as cancer vaccines that protect the recipient from
 development of cancer. The invention provides: vectors and host cells
 (also useful as vaccines); a method of diagnosis of cancer or precancer;
 a transgenic animal; antisense oligonucleotides that inhibit expression
 of the cancer peptide or tumour antigen; antibodies reacting with the CAG
 -3 cancer peptide, useful in diagnostic assays; and methods
 for preventing or inhibiting cancer by administering a cancer peptide,
 with or without an HLA molecule. The cancer peptides form part of, or are
 derived from, cancers such as primary or metastatic melanoma, thyroid,
 lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 treated by inducing cancer-specific T cells in vitro for subsequent
 return to a patient

XX SQ Sequence 180 AA;
 Query Match Score 100.0%; Score 107; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAAARASGPGGAPR 20
 Db 43 RGPRGAAARASGPGGAPR 62

RESULT 5
 AAY52430 standard; protein; 180 AA.

XX ID AAY52430
 XX DT 15-FEB-2000 (first entry)
 AC AAY52430;
 XX
 Human tumour antigen NY-Eso-1.
 DE XX
 KW Cancer; tumour; antigen; MHC; major histocompatibility complex; T-cell;
 KW cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
 KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
 KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
 XX OS Homo sapiens.
 PH Key Location/Qualifiers
 FT Peptide 44..53 /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 60..69 /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 60..68 /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 63..72 /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 79..88 /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 79..87 /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 82..91 /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 82..90 /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 83..91 /note= "Peptide presented by MHC Class I HLA-B44"
 FT Peptide 84..92 /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
 and HLA-B35"
 FT Peptide 87..96 /note= "Peptide presented by MHC Class I HLA-A1"
 FT Peptide 88..96 /note= "Peptide presented by MHC Class I HLA-B44"
 FT Peptide 96..104 /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 100..108 /note= "Peptide presented by MHC Class I HLA-B44"
 FT Peptide 102..110 /note= "Peptide presented by MHC Class I HLA-B44"
 FT Peptide 107..116 /note= "Peptide presented by MHC Class I HLA-A24"
 FT Peptide 110..118 /note= "Peptide presented by MHC Class I HLA-B52"
 FT Peptide 113..122 /note= "Peptide presented by MHC Class I HLA-B7 and HLA-
 B52"
 FT Peptide 113..121 /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 115..124 /note= "Peptide presented by MHC Class I HLA-A3"
 FT

FT	Peptide	118-.126		Best Local Similarity 100 %; Pred. No. 5.6e-05;
FT	Peptide	124-.133	/note= "Peptide presented by MHC Class I HLA-B35"	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT	Peptide	125-.133	/note= "Peptide presented by MHC Class I HLA-B52"	
FT	Peptide	128-.147	/note= "Peptide presented by MHC Class I HLA-A24"	
FT	Peptide	139-.147	/note= "Peptide presented by MHC Class I HLA-B8"	
FT	Peptide	145-.153	/note= "Peptide presented by MHC Class I HLA-B7"	
FT	Peptide	152"	/note= "Peptide presented by MHC Class I HLA-A24 and HLA-B52"	
FT	Peptide	153-.162	/note= "Peptide presented by MHC Class I HLA-B52"	
FT	Peptide	154-.163	/note= "Peptide presented by MHC Class I HLA-B52"	
FT	Peptide	154-.162	/note= "Peptide presented by MHC Class I HLA-B52"	
FT	Peptide	156-.167	/note= "Peptide presented by MHC Class I HLA-B52"	
FT	Peptide	A2"	/note= "Peptide (AYA52434) presented by MHC Class I HLA-A2"	
FT	Peptide	158-	/note= "Peptide presented by MHC Class I HLA-A3"	
FT	Peptide	159-.167	/note= "Peptide presented by MHC Class I HLA-A3"	
FT	Peptide	162-.170	/note= "Peptide presented by MHC Class I HLA-B52"	
XX	W09953938-A1.			
XX	28-OCT-1999.			
XX	24-MAR-1999;	99WO-US006875.		
XX	17-APR-1998;	98US-00062422.		
PR	02-OCT-1998;	98US-00165546.		
PA	(LUDW-D)	LUDWIG INST CANCER RES.		
PI	Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;			
PI	Gure A, Ritter G;			
XX	WPI: 2000-033483/03.			
DR	N-PDBB; AA2Z3880.			
XX	Novel Peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.			
PT	This sequence represents a human tumour antigen, NY-ESO-1, the cDNA encoding which is isolated from an oesophagus squamous cell cancer library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens. Expression in other tumour types being sporadic. Peptides derived from NY-ESO-1 are bound by both MHC (major histocompatibility complex) Class I and Class II molecules for presentation to T-cells. Peptides AAY52431- Y52434 bind to Class I HLA-A2 molecules, thereby stimulating cytotoxic T-cells, while peptides AY52435-Y52440 bind to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation. The peptides derived from NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells.			
SQ	Sequence 180 AA;			
SQ	100.0% ; Score 107; DB 3; Length 180;			
CC	Query Match 100 %; Score 107; DB 3;			
CC	Best Local Similarity 100 %; Pred. No. 5.6e-05;			
CC	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
CC	1 RGPGRGAAARASPGGGGAPR 20			
CC	43 RGPGRGAAARASPGGGGAPR 62			
CC	RESULT 7			
CC	AB03154 standard; protein; 180 AA.			

XX AAB03154; XX 23-OCT-2000 (first entry)

XX Human oesophageal cancer-associated antigen NY-ESO-1.

XX Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;

XX oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;

XX antibody; diagnostic marker; drug delivery target.

XX OS Homo sapiens.

XX Key Location/Qualifiers

PT Modified-site 7 /note= "Potential N-myristoylation site"

PT Modified-site 9 /note= "Potential N-myristoylation site"

PT Modified-site 11 /note= "Potential O-phosphorylation site"

PT Modified-site 98 /note= "Potential O-phosphorylation site"

PT Modified-site 134 /note= "Potential O-phosphorylation site"

PT Modified-site 138 /note= "Potential O-phosphorylation site"

PT Domain 152 .172 /note= "Potential transmembrane domain"

XX US6069233-A.

XX PD 30-MAY-2000.

XX PF 26-JAN-1998; 98US-00013150.

XX PR 03-OCT-1996; 96US-00725181.

XX PA (SLOC) SLOAN KETTERING INST CANCER RES.

XX PA (CORR) CORNELL RES FOUND INC.

XX PA (LUDW) LUDWIG INST CANCER RES.

XX PI Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M; Old LJ; DR; WPI: 2000-410880/35.

XX DR; N-PSDS; AAB61483.

XX PT New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions e.g. infections and cancer.

PS Example 5; Fig 3; 9pp; English.

XX This sequence represents a human oesophageal cancer-associated antigen, PT produced from a specimen of well-to-moderately differentiated squamous cell cancer of the oesophagus. Expression analysis demonstrated CC that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma CC cell lines and in normal ovary and testis tissue but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence CC of the protein indicates that the protein has a transmembrane domain, several N-myristoylation sites and O-phosphorylation sites and that it CC contains antigenic sequences in the N-terminal half of the protein. The CC antigen is useful as an immunogen when combined with an adjuvant, in both CC precursor and post-translationally modified forms, and may be used to CC generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic CC marker for oesophageal cancer, and can be utilised as a marker for the CC targeted delivery of therapeutic agents to oesophageal cancer cells. It CC can also be used to generate diagnostic or therapeutic agents

SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 3; Length 180;

Best Local Similarity 100.0%; Pred. No. 5.6e-05; Mismatches 0; Indels 0; Gaps 0;

DB 43 RGPRGAAARASPGCGGAPR 20

RESULT 8

Qy ID AAB69946 standard; protein; 180 AA.

XX AC AAB69946;

XX DT 27-APR-2001 (first entry)

XX DE Human NY-ESO-1 protein.

XX KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell; HLA-A2; HLA-DR3; melanoma; adenocarcinoma; bladder carcinoma; non-small cell lung carcinoma; tumour status determination.

XX OS Homo sapiens.

XX PN WC200107917-A1.

XX PD 01-FEB-2001.

XX PP 14-JUL-2000; 2000WKO-US019220.

XX PR 23-JUL-1999; 99US-00359503.

XX PA (LUDW) LUDWIG INST CANCER RES.

XX PA (SLOC) SLOAN KETTERING INST CANCER RES.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M; DR; WPI: 2001-182822/18.

XX DR; N-PSDB; AAP58634.

XX PT Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining PT the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.

XX PS Example 5; Fig 3; 50pp; English.

XX CC The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a carcinoma, adenocarcinoma, non-small cell lung carcinoma or bladder carcinoma.

SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 4; Length 180;

Best Local Similarity 100.0%; Pred. No. 5.6e-05; Mismatches 0; Indels 0; Gaps 0;

DB 43 RGPRGAAARASPGCGGAPR 20

RESULT 9

Qy ID AAB69946 standard; protein; 180 AA.

XX AC AAB69946;

XX DT 27-APR-2001 (first entry)

XX DE Human NY-ESO-1 protein.

XX KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell; HLA-A2; HLA-DR3; melanoma; adenocarcinoma; bladder carcinoma; non-small cell lung carcinoma; tumour status determination.

XX OS Homo sapiens.

XX PN WC200107917-A1.

XX PD 01-FEB-2001.

XX PP 14-JUL-2000; 2000WKO-US019220.

XX PR 23-JUL-1999; 99US-00359503.

XX PA (LUDW) LUDWIG INST CANCER RES.

XX PA (SLOC) SLOAN KETTERING INST CANCER RES.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M; DR; WPI: 2001-182822/18.

XX DR; N-PSDB; AAP58634.

XX PT Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining PT the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.

XX PS Example 5; Fig 3; 50pp; English.

XX CC The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a carcinoma, adenocarcinoma, non-small cell lung carcinoma or bladder carcinoma.

SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 3; Length 180;

AAG67164
 ID AAG67164 standard; protein; 180 AA.
 XX
 AC AAG67164;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 DB Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
 XX
 KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
 HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
 cancer; testis tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200162917-A1.
 XX
 PD 30-AUG-2001.
 XX
 PP 22-JAN-2001; 2001WO-US002126.
 XX
 PR 22-FEB-2000; 2000US-00510635.
 XX
 (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Lethe B., Boon-Fallier T.;
 DR WPI: 2001-550091/61.
 DR N-PSDB; AA575118.
 XX
 PT Genomic sequences of tumor associated antigen NY-ESO-1 (LAGE-2) useful
 for diagnosing testicular tumors.
 XX
 PS Example 5: Fig 3; Sopp; English.
 XX
 CC The present sequence represents cancer testis tumour antigen NY-ESO-1
 (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
 least one human leukocyte antigen (HLA) binding peptide, which binds to
 Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
 expressed in tumour mRNA and in testis, but not normal colon, kidney,
 liver or brain tissue. The presence or level of expression of NY-ESO-1
 may be assayed for the diagnosis of cancer, especially testis tumours.
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPGRGAGARASPGGGGAPR 20
 Db 43 RGPGRGAGARASPGGGGAPR 62

RESULT 10
 AAU01535
 ID AAU01535 standard; protein; 180 AA.
 XX
 AC AAU01535;
 XX
 DT 18-JUL-2001 (first entry)
 XX
 DE Human NY-ESO-1 tumour rejection antigen precursor protein.
 KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

PT Modified-site 7 /note= "Myristoylated"
 FT Modified-site 9 /note= "Myristoylated"
 FT Modified-site 11 /note= "Phosphorylated"
 FT Modified-site 98 /note= "Phosphorylated"
 FT Modified-site 134 /note= "Phosphorylated"
 FT Modified-site 138 /note= "Phosphorylated"
 FT Modified-site 138 /note= "Phosphorylated"
 XX
 PN WO200123560-A2.
 XX
 PD 05-APR-2001.
 XX
 PP 26-SEP-2000; 2000WO-US026411.
 XX
 PR 29-SEP-1999; 99US-00408036.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Tureci O., Sahin U., Pfreundschuh M.;
 XX
 DR WPI: 2001-266156/27.
 XX
 DR N-PSDB; AA50254.

XX
 PT Polypeptides binding to major histocompatibility complex class II human
 leukocyte antigen-determining region molecule having amino acid sequence
 found in tumor rejection antigen precursor used for stimulating
 proliferation of helper T cells.

XX
 PS Claim 4; Fig 3; 62pp; English.

XX
 CC The sequence represents a human NY-ESO-1 tumour rejection antigen
 precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
 major histocompatibility complex (MHC) Class II molecules such as human
 leukocyte antigen-determining region (HLA-DR) molecules and stimulate
 proliferation of helper T cells. The peptides can be administered to an
 MHC Class II HLA-DR positive subject in order to stimulate the helper T cells. An MHC
 Class II HLA-DR/NY-ESO-1/SSX-2 complex expressed on the surface of a cell
 or present in free form is useful for this stimulation. The nucleic acid
 sequence is useful for screening for a cancerous condition, which involves
 contacting a subject sample to a cell line transfected with the
 immunoreactive cell (helper T cell), where interaction is indicative of
 cancer. In addition, a sample from a patient (for example, a body fluid
 or tissue) can be monitored for the amount of the complex present in the
 bloodstream. This is useful for determining regression, progression or
 onset of a cancerous condition. The method involves contacting the sample
 with a radioactive labelled or enzyme labelled monoclonal antibody which
 specifically binds with the complex.

XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPGRGAGARASPGGGGAPR 20
 Db 43 RGPGRGAGARASPGGGGAPR 62

RESULT 11
 AAU07714
 ID AAU07714 standard; protein; 180 AA.
 XX
 AC AAU07714;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human NY ESO-1 protein.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 XX NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
 XX immunotherapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155193-A2.
 XX
 PD 02-AUG-2001.
 XX
 PR 26-JAN-2001; 2001WO-US002765.
 XX
 PR 28-JAN-2000; 2000US-0173904P.
 XX
 PR 29-SEP-2000; 2000US-0237107P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wang R, Rosenberg SA, Zeng G;
 XX
 DR WPI; 2001-496851/54.
 XX
 DR N-PSDB; AAD14179, AAD14180.
 XX
 PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.
 XX
 PS Example 1; Fig 1; 134pp; English.
 XX
 The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC protein.
 XX
 SQ Sequence 180 AA;
 XX

Query Match Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGPRGAGAAARASGPGGGAPR 20
 Db 43 RGPRGAGAAARASGPGGGAPR 62

RESULT 12
 AAU84818 AAU84818 standard; protein; 180 AA.
 XX AC AAU11543
 XX DT 08-MAY-2002 (first entry)
 XX DE Human NTNNSOla consensus sequence.

XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
 KW viral infection; human immunodeficiency virus; melanoma;
 KW bacterial infection; Salmonella; Legionella; Giardia.
 KW Trypanosoma; Toxoplasma.
 XX
 OS Homo sapiens.
 XX
 PN WO2001190197-A1.
 XX
 PD 29-NOV-2001.
 XX
 PP 25-MAY-2001; 2001WO-AU000622.
 XX
 PR 26-MAY-2000; 2000AU-0000761.
 XX
 PA (AUTSU) UNIV AUSTRALIAN NAT.
 XX
 PI Thomson SA, Ramshaw IA;
 XX
 DR WPI; 2002-147575/19.
 XX
 PT New synthetic polypeptides having several different segments of at least
 PT one parent polypeptide linked together differently compared to the
 PT linkage in the parent polypeptide, for inducing immune response against a
 PT pathogen or cancer.
 XX
 PS Example 3; Fig 27; 364pp; English.
 XX
 CC The invention relates to a new synthetic polypeptide (I) comprising
 CC several different segments of at least one parent polypeptide linked
 CC together in a different relationship relative to their linkage in the
 CC parent polypeptide to impede, abrogate or otherwise alter at least one
 CC function associated with the parent polypeptide and for inducing an
 CC immune response against a pathogen or cancer. Also included are a
 CC synthetic polypeptides and polymucleotides encoding and a computer system for designing the
 CC synthetic polypeptides and polymucleotides. The synthetic polypeptides and polymucleotides
 CC are referred to as Savine. The synthetic polypeptide is useful for
 CC modulating immune responses preferably directed against a pathogen or a
 CC cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head
 CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
 CC esophagus, brain, testicle, uterus, as potentiating agents.
 CC Compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human
 CC immunodeficiency virus), hepatitis, Japanese encephalitis
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus
 CC Salmonella, Streptococcal, Legionella, and Mycobacterium or parasitic
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
 CC a consensus sequence for a parent protein used to design a Savine of the
 CC invention.
 XX
 SQ Sequence 180 AA;

Query Match Score 107; DB 5; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RGPRGAGAAARASGPGGGAPR 20
 Db 43 RGPRGAGAAARASGPGGGAPR 62

RESULT 13
 AAU11543 AAU11543 standard; protein; 180 AA.
 XX AC AAU11543
 XX DT 12-MAR-2002 (first entry)
 XX DE Human tumour associated antigen NY-ESO.

XX Human; tumour associated antigen; NY-ESO; human leukocyte antigen; NY-ESO; human leukocyte antigen; MHC; HLA-A2; 2; vaccine; cancer; HIV;
 XX major histocompatibility complex; HLA-A2; 2; vaccine; cancer; HIV;
 XX human immunodeficiency virus infection; cytostatic; virucide;
 XX housekeeping epitope; adoptive immunotherapy; neoplastic disease;
 XX viral disease; hepatitis virus; papilloma virus; tumour; leukaemia;
 XX lymphoma; breast cancer; prostate cancer; lung cancer;
 XX parasitic infection; Chlamydia; Trypanosoma; Toxoplasma.
 XX Homo sapiens.

XX WO200188963-A2.

XX 08-NOV-2001.

XX PD NOV-2001; 2001WO-US013806.

XX 27-APR-2001; 2000US-00561045.

XX 28-APR-2000; 2000US-00561074.

XX 28-APR-2000; 2000US-00561571.

XX 28-APR-2000; 2000US-00561572.

XX (CTLI-) CTL IMMUNOTHERAPIES CORP.

XX Simard JJL, Diamond DC, Lei X;

XX PI; 2002-066492/09.

XX Novel vaccine useful for treating neoplastic and viral diseases, comprising a first housekeeping epitope derived from a first antigen associated with a first target cell.

XX Example 23: Fig 17; 131pp; English.

XX The invention relates to a vaccine comprising a first housekeeping epitope derived from a first antigen associated with a first target cell. Also included are an isolated T cell expressing a T cell receptor specific for a major histocompatibility complex (MHC)-peptide complex comprising a first housekeeping epitope which is derived from a first antigen associated with a first target cell, selecting an epitope (or peptide sequence) from a population of peptide fragments of an antigen associated with a target in a host, where the fragments have a known or predicted affinity for a MHC receptor peptide binding cleft of the host, where the epitope selected corresponds to a product of proteolytic cleavage of the antigen in a cell of the host and a nucleic acid construct comprising a first coding region, where the first coding region comprises a first sequence encoding at least a first polypeptide, where the first polypeptide comprises a first housekeeping epitope derived from a first antigen associated with a first target cell; the epitopes, peptides, vaccines and nucleic acids are useful in the manufacture of a medicament for use in adoptive immunotherapy and for prevention and treatment of neoplastic and viral diseases (e.g., human immunodeficiency virus, HIV, infection, hepatitis virus and papilloma virus), cancers (e.g., tumours, leukaemia, lymphoma, breast cancer, prostate cancer and lung cancer), infection of cells by intracellular parasites (e.g., Chlamydia, Trypanosoma and Toxoplasma) and many other examples given in the specification. The invention permits the vaccine designer to ignore peptides that, despite predicted high binding affinity for MHC, will never be useful because they cannot be presented by target cells. The invention provides a major advance in vaccine design, one that combines the power of antigen sequence analysis with the fundamental realities of immunology. The invention allows for the simple and effective selection of meaningful epitopes for creation of MHC class I or Class II vaccines using any polypeptide sequence corresponding to a desired target. The present sequence is an HLA-A2.1 (human leukocyte antigen) presenting target cell protein from which epitopes of the invention may be derived, CC Sequence 180 AA;

XX Sequence 180 AA;

CC Query Match 100.0%; Score 107; DB 5; Length 180;
 CC Best Local Similarity 100.0%; Prd. No. 5.6e-05; Pred. No. 5.6e-05;
 CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARANGPGCGGAPR 20
 Db 43 RGPRGAGAARANGPGCGGAPR 62

RESULT 14
 ID ABR58672 standard; protein; 180 AA.

XX

AC ABR58672;

XX DT 09-JUL-2003 (first entry)

XX DE Human cancer related protein SEQ ID NO:329.

XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.

XX OS Homo sapiens.

XX PN WO2003025138-A2.

XX PD 27-MAR-2003.

XX PP 17-SEP-2002; 2002WO-US029560.

XX PR 17-SEP-2001; 20061US-0323469P.

XX PR 20-SEP-2001; 20061US-0323487P.

XX PR 13-NOV-2001; 20061US-0350666P.

XX PR 08-FEB-2002; 20062US-0355145P.

XX PR 08-FEB-2002; 20062US-0355572P.

XX PR 12-APR-2002; 20062US-037246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KB; Zlotnick A;

XX DR WPI; 2003-354660/33. N-PSDB; ACC72823.

XX New genes that are up-regulated or down-regulated in cancers, useful as PT markers for diagnosing e.g. cancer, ischaemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases. PS Claim 12; Page 757-758; 76pp; English.

XX The present invention describes an isolated nucleic acid molecule, which CC comprises the sequence of any of the genes that are up-regulated or down- CC regulated in specific cancers (e.g., about 1031 genes up-regulated in CC acute lymphocytic leukemia). ACC72841 to ACC72860 represent cancer CC related gene nucleotide sequences which encode the proteins given in CC ACC72821 to AB58709. Also described is (1) determining the presence or CC absence of a pathological cell in a patient; (2) an expression vector CC comprising a nucleic acid molecule described above; (3) a host cell CC comprising the vector; (4) an isolated polypeptide, which is encoded by CC the nucleic acid; (5) an antibody that specifically binds the polypeptide CC of (4); (6) specifically targeting a compound to a pathological cell in a CC patient by administering the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or CC therapeutic targets. In particular, the nucleic acid is useful for CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, CC bladder, brain, breast, cervix, colon, rectum, kidney, lung, ovary, CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, CC atherosclerosis and endometriosis. The nucleic acid is also useful in CC drug screening, particularly for identifying agents for treating these CC pathologies

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 6; Length 180;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Pred. No. 5.6e-05;

```

Matches      20;   Conservative      0;   Mismatches      0;   Indels      0;   Gaps      0;
Mismatches      1   RSPRGAGAARASPGGGAPR 20
Indels      43   RSPRGAGAARASPGGGAPR 62
Gaps      0;   Job time : 71.6667 secs
Search completed: June 22, 2004, 08:51:24

```

RESULT 15
ABR4810
D PBR4B210 standard; protein; 180 AA.
X
C ABR4B210;
X
X
T 12-JUN-2003 {first entry}
X Human bladder cancer associated protein sequence SEQ ID NO:159.
X WO2003003906-A2.
X Human; bladder cancer; cytostatic; gene therapy; vaccine.
X
Homo sapiens.
X
X
X
D 16-JAN-2003.
X
X
P 03-JUL-2002; 2002WO-US021338.
X
P 03-JUL-2001; 2001US-0302B14P.
P 03-AUG-2001; 2001US-0310099P.
P 08-NOV-2001; 2001US-034370P.
P 13-NOV-2001; 2001US-0350666P.
P 12-APR-2002; 2002US-037224F.
X
PA EOS BIOTECHNOLOGY INC.
PA Mack DH, Aziz N;
PA

RESULT 2
US-09-392-714-25
Sequence 25, Application US/09392714A
Patent No. 6686147

GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Gure, Ali O.
APPLICANT: Williamson, Barbara
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Cancer Associated Antigens and Uses
FILE REFERENCE: L04617/7062

CURRENT APPLICATION NUMBER: US/09/392,714A
EARLIER FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 30
SEQ ID NO: 25
TYPE: PRT
ORGANISM: Homo sapiens
US-09-392-714-25

Query Match 100.0% Score 107; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAASPGGGAPR 20
Db 43 RAPRGAGAAASPGGGAPR 62

RESULT 3
US-09-937-263B-8
Sequence 8, Application US/08937263B
Patent No. 6274115

GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Knutl, Alexander; Old, Lloyd J.;
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESS: Fullbright & Jaworski, L.L.P.,
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/937263B
FILING DATE: September 15, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 180
TOPOLOGY: linear

Query Match 94.4% Score 101; DB 4; Length 180;
Best Local Similarity 95.0%; Pred. No. 9.9e-05;
Matches 19; Conservative 0; Indels 1; Gaps 0;

Qy 1 RGPRGAGAAASPGGGAPR 20
Db 43 RAPRGAGAAASPGGGAPR 62

RESULT 5
US-08-791-495-7
Sequence 7, Application US/08791495
Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Lech , Bernard
APPLICANT: Lucas , Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Danielle
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 10461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-495-7

Query Match 92.5%; Score 99; DB 2; Length 210;
Best Local Similarity 95.0%; Pred. No. 0.00019;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAPR 20
Db 43 RGPRGAGAARASGPGGGAPR 62

RESULT 6
US-08-791-495-5
Sequence 5, Application US/08791495
Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Lech , Bernard
APPLICANT: Lucas , Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Danielle
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

Query Match 92.5%; Score 99; DB 2; Length 180;
Best Local Similarity 95.0%; Pred. No. 0.00017;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAPR 20
Db 43 RGPRGAGAARASGPGGGAPR 62

RESULT 7
US-09-252-991A-25681
Sequence 23681, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074, 788
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25681
LENGTH: 860
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25681

Query Match 92.5%; Score 99; DB 4; Length 860;
Best Local Similarity 95.0%; Pred. No. 8.2%;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAP 19
Db 738 RRGGSTAATGCGGGT 756

RESULT 8
US-09-252-991A-27091
Sequence 27091, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252, 991A
CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 27091
LENGTH: 160

TYPE: PRT
ORGANISM: *Pseudomonas aeruginosa*
US-09-255-991A-27091

Query Match 56.1%; Score 60; DB 4; Length 160;
Best Local Similarity 6.6%; Pred. No. 3.8;
Matches 14; Conservative 0; Mismatches 4; Indels 4; Gaps 1;
Qy 3 PRGAGAARASG---PGGGAPR 20
Db 103 PRGAGAARASGRCRPAPGPR 124

RESULT 9

US 08-442-248-2
Sequence 2, Application US/08442248
Patent No. 5798448
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
ZIP: 94098

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,815
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 920C1
REFERENCE DOCKET NUMBER: 920C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-3881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-440-815-2

Query Match 56.1%; Score 60; DB 1; Length 928;
Best Local Similarity 61.9%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGAARASGPGGG--APR 20

Db 5 GPRGAGAARRTQGRGGGDTPR 25

RESULT 11
US-08-440-815-2
Sequence 2, Application US/08440815
Patent No. 6280732
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
ZIP: 94098

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:

Query Match 56.1%; Score 60; DB 1; Length 928;
Best Local Similarity 61.9%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGAARASGPGGG--APR 20

Db 5 GPRGAGAARRTQGRGGGDTPR 25

RESULT 10

APPLICATION NUMBER: US/08/486,449

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/330128

FILING DATE: 27-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 415/225-9881

TELEX: 910/371-7168

SEQUENCE CHARACTERISTICS:

LENGTH: 928 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-486-449-2

Query Match 56.1%; Score 60; DB 3; Length 928;
Best Local Similarity 61.9%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGARASGPGG--APR 20

Db 5 GPRGAGRRRTQGRGGGDTPR 25

RESULT 12
US-08-578-684-2

Sequence 2, Application US/08578684

Patent No. 6610296

GENERAL INFORMATION:

APPLICANT: Caras, Ingrid W.

APPLICANT: Winslow, John W.

TITLE OF INVENTION: AL-1 Neurotrophic Factor

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winfatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/578,684

FILING DATE: 02-Jan-1996

CLASSIFICATION: 514

PRIOR APPLICATION:

APPLICATION NUMBER: 08/330128

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/466449

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 928 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-578-684-2

Sequence 10, Application US/08469537A

Patent No. 5843749

GENERAL INFORMATION:

APPLICANT: Maissonpierre, et al.

TITLE OF INVENTION: EHk AND RrR TYROSINE

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill River Road

CITY: Tarrytown

STATE: NY

COUNTRY: U.S.A.

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,537A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/406,247

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: USN 08/144,992

FILING DATE: 28-OCT-1993

APPLICATION NUMBER: USN 07/736,559

FILING DATE: 26-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: Kempfer, Ph.D., Gail M

REGISTRATION NUMBER: 32,143

REFERENCE/DOCKET NUMBER: REG 070C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 914-345-7721

TELEFAX: 914-345-7721

TELEX:

INFORMATION FOR SEQ ID NO: 103:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-469,537A-103

Query Match 56.1%; Score 60; DB 2; Length 1005;

Best Local Similarity 61.9%; Pred. No. 21;

Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGARASGPGG--APR 20

Db 5 GPRGAGRRRTQGRGGGDTPR 25

RESULT 13

US-08-469-537A-103

Sequence 10, Application US/08469537A

Patent No. 5843749

GENERAL INFORMATION:

APPLICANT: Maissonpierre, et al.

TITLE OF INVENTION: KINASES

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill River Road

CITY: Tarrytown

STATE: NY

COUNTRY: U.S.A.

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,537A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/406,247

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: USN 08/144,992

FILING DATE: 28-OCT-1993

APPLICATION NUMBER: USN 07/736,559

FILING DATE: 26-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: Kempfer, Ph.D., Gail M

REGISTRATION NUMBER: 32,143

REFERENCE/DOCKET NUMBER: REG 070C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 914-345-7721

TELEFAX: 914-345-7721

TELEX:

INFORMATION FOR SEQ ID NO: 103:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-469-537A-103

Query Match 56.1%; Score 60; DB 2; Length 1005;

Best Local Similarity 61.9%; Pred. No. 21;

Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGARASGPGG--APR 20

Db 5 GPRGAGRRRTQGRGGGDTPR 25

RESULT 14

US-08-252-991b-24923

Sequence 2423, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT PUBLISHING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 4923
 LENGTH: 210
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24923

Query Match 55.1%; Score 59; DB 4; Length 210;
 Best Local Similarity 70.6%; Pred. No. 6.4;
 Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 4 RGAGAAARASGPGGGAPR 20
 Db 154 RFACTAAADGAGGCAAPR 170

RESULT 15
 US 08-118-270-21
 Sequence 21, Application US/08118270
 Patent No. 550884
 GENERAL INFORMATION
 APPLICANT: Murphy, Randall B.
 APPLICANT: Schusser, David I.
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWNDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.2.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/118,270

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY=2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEX: 248633

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 330 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-118-270-21

Query Match 55.1%; Score 59; DB 1; Length 330;
 Best Local Similarity 55.0%; Pred. No. 9.6;

Matches 11; Conservative 2; Mismatches 7;
 Indels 0; Gaps 0;
 Qy 1 RGPRGAAARASGPGGGAPR 20
 Db 212 RRPNGLGPERSAGPGGRGR 231

Search completed: June 22, 2004, 08:54:48
 Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:51:28 ; Search time 52 Seconds
 108.582 Million cell updates/sec

Title: US-09-529-206D-4_COPY_43_62
 Perfect score: 107
 Sequence: 1 RPRGAGARASSGGGAPR 20

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	107	100.0	180	10 US-09-849-602-30	Sequence 30, App
2	107	100.0	180	12 US-10-296-734-132	Sequence 832, App
3	107	100.0	180	14 US-10-207-655-71	Sequence 71, App
4	107	100.0	180	15 US-10-026-066-3	Sequence 3, App
5	107	100.0	180	15 US-10-117-937-74	Sequence 74, App
6	107	100.0	180	15 US-10-295-027-386	Sequence 386, App
7	107	100.0	180	16 US-10-188-832-139	Sequence 139, App
8	107	100.0	397	9 US-09-821-983-27	Sequence 27, App
9	102	95.3	30	12 US-10-296-734-1404	Sequence 1404, App
10	102	95.3	3541	12 US-10-296-734-1454	Sequence 1454, App
11	101	94.4	180	9 US-09-751-798-8	Sequence 8, App
12	101	94.4	180	13 US-10-023-182-8	Sequence 8, App
13	101	94.4	180	14 US-10-364-614-14	Sequence 14, App
14	99	92.5	135	15 US-10-295-027-386	Sequence 386, App
15	99	92.5	135	16 US-10-188-832-141	Sequence 141, App

ALIGNMENTS

RESULT 1
 US-09-849-602-30
 ; Sequence 30, Application US/09849602
 ; Publication No. US20030165834A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Scanlan, Matthew J.
 ; ATTORNEY: Old, Lloyd J.
 ; APPLICANT: Stockert, Elisabeth
 ; APPLICANT: Chen, Yao-Tseng
 ; TITLE OF INVENTION: Colon Cancer Antigen Panel
 ; FILE REFERENCE: L0461-7105 (TRV)
 ; CURRENT APPLICATION NUMBER: US/09-849-602
 ; CURRENT FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 30
 ; LENGTH: 180
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-849-602-30

Query Match 100.0%; Score 107; Best Local Similarity 100.0%; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGFRGAGAARASGGGAPR 20
 Ds 43 RGFRGAGAARASGGGAPR 62

RESULT 2
 US-10-296-734-832
 ; Sequence 832, Application US/10296734
 ; Publication No. US20040054137A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Scott A
 ; ATTORNEY: Ramsay, Ian A
 ; TITLE OF INVENTION: Synthetic molecules and uses therefor

```

FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU FQ7761/00

PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: Patentin version 3.2
SEQ ID NO: 832
LENGTH: 180
TYPE: PRT
ORGANISM: Artificial

OTHER INFORMATION: NYNSOLA consensus polypeptide
US-10-296-734-832

Query Match 1 RGPGRGAGARASGPGGAPR 20
Score 100; DB 12; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Query Match 1 RGPGRGAAARSGPGGAPR 20
Score 100.0%; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

RESULT 5
US-10-117-937-74
Sequence 74, Application US/10117937
Publication No. US20030220239A1
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
SIMARD, John, J.L.
DIAMOND, David, C.
LIU, Liping
XIE, Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTIIM-027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FastSBQ for Windows Version 4.0
SEQ ID NO: 74
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 1 RGPGRGAGARASGPGGAPR 20
Score 100.0%; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Query Match 1 RGPGRGAAARSGPGGAPR 20
Score 100.0%; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

RESULT 6
US-10-295-027-386
Sequence 386, Application US/10295027
Publication No. US2003023230A1
GENERAL INFORMATION:
AFAR, Daniel
Aziz, Natasha
Ginsberg, Wendy M.
Gish, Kurt C.
Glynn, Richard
Hevezi, Peter A.
Mack, David H.
Murray, Richard
Watson, Susan R.
EOS Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US

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CURRENT APPLICATION NUMBER: US/10/295,027
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663,733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335,394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332,464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334,393
 PRIOR FILING DATE: 2001-11-39
 PRIOR APPLICATION NUMBER: US 60/340,376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347,211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347,349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355,250
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: US 60/356,714
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PAlM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 386
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-295-027-386

Query Match 100.0%; Score 107; DB 15; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.00033; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAAARASGPGGGAPR 20
 Db 43 RGPRGAAARASGPGGGAPR 62

RESULT 7
 US-10-188-832-139

Sequence 139, Application US/10/88832
 Publication No. US20040076955A1
 GENERAL INFORMATION:
 APPLICANT: Mack, David H.
 AZIZ, Nacissa
 APPLICANT: Eos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
 and Methods of Screening for Modulators of Bladder Cancer
 FILE REFERENCE: 018501-002330US
 CURRENT FILING DATE: 2002-11-22
 PRIOR APPLICATION NUMBER: US 60/302,814
 PRIOR FILING DATE: 2001-07-03
 PRIOR APPLICATION NUMBER: US 60/310,099
 PRIOR FILING DATE: 2001-08-03
 PRIOR APPLICATION NUMBER: US 60/343,705
 PRIOR FILING DATE: 2001-11-08
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/372,246
 NUMBER OF SEQ ID NOS: 207
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 139
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-188-832-139

Query Match 100.0%; Score 107; DB 16; Length 180;

RESULT 8
 US-09-821-883-27
 Sequence 27, Application US/09821883
 Patent No. US20020061310A1
 GENERAL INFORMATION:
 APPLICANT: Laus, Reiner
 APPLICANT: Vidovic, Damir
 APPLICANT: Graddis, Thomas
 TITLE OF INVENTION: Compositions and Methods for Dendritic
 Cell-Based Immunotherapy
 FILE REFERENCE: 7635-0022.30
 CURRENT APPLICATION NUMBER: US/09/821,883
 CURRENT FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: US 60/193,504
 PRIOR FILING DATE: 2000-03-30
 NUMBER OF SEQ ID NOS: 30
 SEQ ID NO: 27
 LENGTH: 397
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: NY-ESO-IC tumor antigen
 US-09-821-883-27

Query Match 100.0%; Score 107; DB 9; Length 397;
 Best Local Similarity 100.0%; Pred. No. 0.00065; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAAARASGPGGGAPR 20
 Db 43 RGPRGAAARASGPGGGAPR 62

RESULT 9
 US-10-296-734-1404

Sequence 1404, Application US/10296734
 Publication No. US20040054137A1
 GENERAL INFORMATION:
 APPLICANT: Thompson, Scott A
 APPLICANT: Ranshaw, Ian A
 TITLE OF INVENTION: Synthetic molecules and uses therefor
 FILE REFERENCE: Savine
 CURRENT FILING DATE: 2003-09-04
 PRIOR APPLICATION NUMBER: AU PQ7761/00
 PRIOR FILING DATE: 2000-05-26
 NUMBER OF SEQ ID NOS: 1507
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 1404
 LENGTH: 30
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: NYS01a segment 4
 US-10-296-734-1404

Query Match 100.0%; Score 102; DB 12; Length 30;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPRGAAARASGPGGGAPR 20
 Db 1 GPRGAAARASGPGGGAPR 19

Query Match 100.0%; Score 102; DB 12; Length 30;

OTHER INFORMATION: NYS01a segment 4

US-10-296-734-1404

Query Match 95.3%; Score 102; DB 12; Length 30;

Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPRGAAARASGPGGGAPR 20
 Db 1 GPRGAAARASGPGGGAPR 19

Query Match 100.0%; Score 102; DB 16; Length 180;

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RESULT 10
US-10-296-734-1454
; Sequence 1454, Application US10296734
; Publication No. US1004005413781
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; CURRENT APPLICATION NUMBER: US10/296,734
; CURRENT FILING DATE: 2003-05-04
; PRIOR APPLICATION NUMBER: AU PCT7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NCS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 1454
; LENGTH: 3541
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Melanoma cancer specific savine
US-10-296-734-1454

Query Match          Score: 102; DB 12; Length: 2377
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 0; Mismatches 0; Indels 0

Qy      2 GPRGAGAARASGGGGGPR 20
        ||||| | | | | | | | | |
Db     2359 GRRGAGAARASGGGGP 2377

RESULT 11
US-09-751-798-8
; Sequence 8, Application US09751798
; Patent No. US20020010321A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Macthew;
; APPLICANT: Knuth, Old; Lloyd, J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 C-Associated Proteins, Uses Thereof, Truncated Forms of NY-ESO-1, and HuT14 Peptides Derived Therefrom
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fabbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020010321A1zen D.
; REGISTRATION NUMBER: 30,946
; REFERENCE DOCKET NUMBER: LUD 5466-3
; TELECOMMUNICATION INFORMATION:
; ENDPOINT: 128.122.128.210

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Db 43 RAPRGAGAARASGPGGGAPR 62

RESULT 13
 US-10-364-614-14
 Sequence 14, Application US/10364614
 Publication No. US2003017520A1
 GENERAL INFORMATION:
 APPLICANT: JAGER, Elke
 APPLICANT: KNUTH, Alexander
 APPLICANT: OLD, Lloyd
 APPLICANT: Gnjetic, Sacha
 FILE REFERENCE: IUD 5526.1 CIP 14
 CURRENT APPLICATION NUMBER: US/10/364,614
 CURRENT FILING DATE: 2003-02-24
 PRIOR APPLICATION NUMBER: US 60/355,828
 PRIOR FILING DATE: 2002-02-13
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 14
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-364-614-14

Query Match 94.4%; Score 101; DB 14; Length 180;
 Best Local Similarity 95.0%; Pred. No. 0.0014;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RGPRGAGAARASGPGGGAPR 20
 Db 43 RAPRGAGAARASGPGGGAPR 62

RESULT 14
 US-10-295-027-388
 Sequence 388, Application US/10295027
 Publication No. US20030232350A1
 GENERAL INFORMATION:
 APPLICANT: Atar, Daniel
 APPLICANT: Ariz, Natasha
 APPLICANT: Ginsberg, Wendy M.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Glynn, Richard
 APPLICANT: Hevezsi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: Eos Biotechnology, INC.
 TITLE OF INVENTION: Methods of Diagnosing of Cancer, Compositions and
 FILE REFERENCE: 018501-012500US
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663,733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335,394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332,464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334,393.
 PRIOR APPLICATION NUMBER: US 60/340,376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347,211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347,349
 PRIOR APPLICATION NUMBER: US 60/355,250
 PRIOR FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: US 60/356,714
 ; PRIOR FILING DATE: 2002-02-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1386
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 388
 ; LENGTH: 135
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-295-027-388

Query Match 92.5%; Score 99; DB 15; Length 135;
 Best Local Similarity 95.0%; Pred. No. 0.0018;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RGPRGAGAARASGPGGGAPR 20
 Db 43 RAPRGAGAARASGPGGGAPR 62

RESULT 15
 US-10-188-832-141
 Sequence 141, Application US/10188832
 Publication No. US20040076955A1
 GENERAL INFORMATION:
 APPLICANT: Aziz, Natasha
 APPLICANT: Eos Biotechnology, Inc.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions and
 Methods of Screening for Modulators of Bladder
 TITLE OF INVENTION: Cancer
 FILE REFERENCE: 018501-002330US
 CURRENT APPLICATION NUMBER: US/10/188,832
 CURRENT FILING DATE: 2002-11-22
 PRIOR APPLICATION NUMBER: US 60/302,814
 PRIOR FILING DATE: 2001-07-03
 PRIOR APPLICATION NUMBER: US 60/310,099
 PRIOR FILING DATE: 2001-08-03
 PRIOR APPLICATION NUMBER: US 60/343,705
 PRIOR FILING DATE: 2001-11-08
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/372,246
 PRIOR FILING DATE: 2002-04-12
 NUMBER OF SEQ ID NOS: 207
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 141
 LENGTH: 135
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-188-832-141

Query Match 92.5%; Score 99; DB 16; Length 135;
 Best Local Similarity 95.0%; Pred. No. 0.0018;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAPR 20
 Db 43 RAPRGAGAARASGPGGGAPR 62

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 Job time : 52 secs

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number of hits satisfying chosen parameters:	281					
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database:	PIR 78: 1: PIR1: 2: PIR2: 3: PIR3: 4: PIR4: *					
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score greater than or equal to the score of the resu-	l					
and is derived by analysis of the total score distribu-	tion					
SUMMARIES						
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3	60	56.1	981	2	S51604	
4	60	56.1	1005	2	S49115	
5	59	55.1	129	1	OTRUBB	
6	59	55.1	877	1	I4997	
7	58.5	54.7	566	2	T21096	
8	58.5	54.7	692	2	T21095	
9	57	53.3	129	1	JC2254	
10	57	53.3	355	2	T36273	
11	56	52.3	331	2	S78452	
12	55	51.4	201	2	C40040	
13	55	51.4	201	2	S26404	
14	55	51.4	248	2	A40040	
15	55	51.4	250	2	T465117	
16	55	51.4	292	2	B40040	
17	55	51.4	1235	2	T32234	
18	54.5	50.9	496	2	F83124	
19	54	50.5	388	2	T29173	
20	54	50.5	597	2	S51112	
21	54	50.5	730	2	A36226	
22	54	50.5	1733	1	B45344	
23	53.5	50.0	627	2	A4112	
24	53.5	50.0	3110	2	T13218	
25	53	49.5	485	1	F71275	
26	53	49.5	1306	2	A70334	
27	52.5	49.1	450	2	A34169	
28	52.5	49.1	782	2	S33945	
29	52.5	49.1	1650	2	T35044	

A; Cross-references: EMBL:U07357; NID:9466369; PIDN:AA17038.1; PID:9466370
 C; Genetics:
 A; Gene: Bsk
 C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 F; 512-528/Domain: protein kinase ATP-binding motif
 F; 801-868/Domain: SAM homology <SAM>
 Query Match 55.1%; Score 59; DB 2; Length 877;
 Best Local Similarity 61.9%; Pred. No. 20;
 Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
 Qy 2 PRGAGAARASGGGG- APR 20
 Db 5 PRGAGAATRTOGRGGDTPR 25

RESULT 7
 T21096 hypothetical protein F18H3.3b - Caenorhabditis elegans
 C; Species: Caenorhabditis elegans
 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C; Accession: T21096
 R; Coles, L.
 Submitted to the EMBL Data Library, July 1995
 A; Reference number: Z19373
 A; Accession: T21096
 A; Status: Preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-566 <WIL>
 A; Cross-references: EMBL:Z00101; PIDN:CAA90446.1; GSPDB:GN00028; CESP:F18H3.3b
 A; Experimental source: Clone F18H3
 C; Genetics:
 A; Gene: CESP:F18H3.3b
 A; Map position: X
 A; Introns: 111/1; 215/2; 469/3; 552/3
 -C; Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
 Query Match 54.7%; Score 58.5; DB 2; Length 566;
 Best Local Similarity 65.0%; Pred. No. 16;
 Matches 13; Conservative 0; Mismatches 4; Indels 3; Gaps 1;
 Qy 3 PRGAGAARASGGP--CCGP 19
 Db 530 PRDAGAPRGGGPVGQMGCGAP 549

RESULT 8
 T21095 hypothetical protein F18H3.3a - Caenorhabditis elegans
 C; Species: Caenorhabditis elegans
 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C; Accession: T21095
 R; Coles, L.
 Submitted to the EMBL Data Library, July 1995
 A; Reference number: Z19373
 A; Status: Preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-692 <WIL>
 A; Cross-references: EMBL:Z50110; PIDN:CAA90444.1; GSPDB:GN00028; CESP:F18H3.3a
 C; Genetics:
 A; Gene: CESP:F18H3.3a
 A; Map position: X
 A; Introns: 111/1; 215/2; 469/3; 552/3
 -C; Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
 Query Match 54.7%; Score 58.5; DB 2; Length 692;
 Best Local Similarity 65.0%; Pred. No. 19;
 Matches 13; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 3 PRGAGAARASGGP--CCGP 19
 Db 530 PRDAGAPRGGGPVGQMGCGAP 549

RESULT 9
 JC2254 cytochrome-c oxidase (EC 1.9.3.1) chain Vb precursor - rat
 N; Alternative names: cytochrome c oxidase (EC 1.9.3.1) chain VIa*
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 28-Oct-1994 #sequence_revision 26-May-1995 #text_change 16-Jun-2000
 C; Accession: JC2254; S63375
 R; Hoshinaga, H.; Amuro, N.; Goto, Y.; Okazaki, T.
 J. Biochem. 115: 194-201, 1994.
 A; Title: Molecular cloning and characterization of the rat cytochrome c oxidase subunit I. A; Reference number: JC2254; PMID:94266742; MUID:8206867
 A; Accession: JC2254
 A; Molecule type: mRNA
 A; Residues: 1-129 <ROS>
 A; Cross-references: DDBJ:D10952; NID:9193694; PIDN:BAK01744.1; PID:9193695
 A; Experimental source: liver
 A; Accession: JC2255
 A; Molecule type: DNA
 A; Residues: 1-129 <HO2>
 A; Cross-references: DDBJ:D10951
 A; Molecule type: DNA
 A; Residues: 1-129 <HO2>
 A; Cross-references: DDBJ:D10951
 A; Molecule type: DNA
 A; Residues: 1-129 <HO2>
 A; Cross-references: DDBJ:D10951
 A; Molecule type: DNA
 A; Residues: 1-129 <HO2>
 A; Cross-references: EMBL:X142008
 R; Schaegger, H.; Noack, H.; HaLangk, W.; Brandt, U.; von Jagow, G.
 Eur. J. Biochem. 230: 235-241, 1995
 A; Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-acid sequence of cDNA for rat liver and brain cytochrome c oxidase subunit I. A; Reference number: S6336668; MUID:89366668; PMID:2549512
 A; Accession: S05318
 A; Molecule type: mRNA
 A; Residues: 31-129 <GOT>
 A; Cross-references: EMBL:X142008
 R; Schaegger, H.; Noack, H.; HaLangk, W.; Brandt, U.; von Jagow, G.
 Eur. J. Biochem. 230: 235-241, 1995
 A; Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-acid sequence of cDNA for rat liver and brain cytochrome c oxidase subunit I. A; Reference number: S63372; MUID:95324529; PMID:7601105
 A; Accession: S5375
 A; Molecule type: protein
 A; Residues: 32-41 <SCH>
 A; Experimental source: liver
 C; Genetics:
 A; Gene: CXVB-1
 A; Introns: 35/1; 59/3; 93/1
 A; Note: intronless gene COXVB-2 apparently a nonfunctional processed pseudogene
 C; Superfamily: mammalian cytochrome-c oxidase chain Vb
 C; Keywords: membrane-associated complex; mitochondrial inner membrane; mitochondrion; o: P; 1-31/Domain: transit peptide
 P; 32-129/Product: cytochrome-c oxidase chain Vb #status predicted <NP>
 P; 32-129/Product: cytochrome-c oxidase chain Vb #status predicted <NP>
 Query Match 53.3%; Score 57; DB 1; Length 129;
 Best Local Similarity 55.6%; Pred. No. 7.4%;
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 Qy 2 GPRGAGAARASGGCGGAP 19
 Db 21 GPRGAGAATRSMASGGCGVP 38

RESULT 10
 T36273 hypothetical protein SCR68.23c - Streptomyces coelicolor
 C; Species: Streptomyces coelicolor
 C; Date: 0-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
 C; Accession: T36273
 R; Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A; Reference number: 221576
 A; Accession: T36273
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-355 <MUR>

A;Cross-references: EMBL:AL079345; PIDN:CAP45359.1; GSPDB:GN00070; SCOEDB:SCE68.23C
 A;Experimental source: strain A3 (2)
 C;Genetics:
 A;Gene: SCOEDB:SC68.23C
 C;Superfamily: Streptocyes coelicolor hypothetical protein SC68.23C

Query Match 53 3%; Score 57; DB 2; Length 355;
 Best Local Similarity 57.9%; Pred. No. 17; Mismatches 7; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAARASGPGGGAP 19
 Db 15 RGSRGTGRGGGGGGGAP 33

RESULT 11
 S73452
 POU domain protein rdc-1 - human
 C;Species: Homo sapiens (man)
 C;Accession: 19-Mar-1998 #sequence revision 19-Mar-1998 #text_change 24-Sep-1999
 R;Alt. F.W.
 Submitted to the EMBL Data Library, February 1999
 A;Reference number: S73452
 A;Accession: S73452
 A;Molecule type: mRNA
 A;Residues: 1-201 <ALT>
 A;Cross-references: EMBL:X64624; NID:935914; PIDN:CAA45907.1; PID:935915
 R;Collum, R.G.; Fisher, P.B.; Datta, M.; Mellis, S.; Thiele, C.; Huebner, K.; Croce, C.M.
 Nucleic Acids Res. 20, 4919-4925, 1992
 A;Title: A novel POU homeodomain gene specifically expressed in cells of the developing
 A;Accession number: 138151; MUID:1357830
 A;Accession: S26063
 A;Molecule type: mRNA
 A;Residues: 174-177,'S',179-233,'K',235-327 <COL>
 A;Experimental source: placenta
 C;Superfamily: unassigned homeobox proteins, homeobox homeoCPY; POU domain homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;181-250/Domain: POU domain homology <POU>
 F;181-324/Domain: homeobox homology <HOX>

Query Match 52 3%; Score 56; DB 2; Length 331;
 Best Local Similarity 61.1%; Pred. No. 20; Mismatches 3; Indels 4; Gaps 1;
 Matches 11; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

Qy 2 GPRGAGAAARASGPGGGAP 19
 Db 65 GPRGGG---GGPGGGG 78

RESULT 12
 C40040
 alternative splicing factor ASF-3 - human
 C;Species: Homo sapiens (man)
 C;Accession: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 03-Dec-1999
 R;Ge, H.; Zuo, P.; Manley, J.L.
 Cell 66, 373-382, 1991
 A;Title: Primary structure of the human splicing factor ASF reveals similarities with Dr
 A;Reference number: A40040; MUID:91309149; PMID:1855527
 A;Accession: C40040
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-248 <GEA>
 A;Accession: C40040
 R;Ge, H.; Zuo, P.; Manley, J.L.
 Cell 66, 373-382, 1991
 A;Title: Primary structure of the human splicing factor ASF reveals similarities with Dr
 A;Reference number: A40040; MUID:91309149; PMID:1855527
 A;Accession: C40040
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-201 <GEA>
 A;Cross-references: GS:MF2709
 C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoproteins
 F;17-81/Domain: ribonucleoprotein repeat homology <RRM1>
 F;122-182/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 51 4%; Score 55; DB 2; Length 201;
 Best Local Similarity 55.0%; Pred. No. 18; Mismatches 9; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 RGRGAGAAARASGPGGGAP 20
 Db 90 RSGRGTGRGGGGGGGAP 109

RESULT 13
 S26404
 alternative splicing factor ASF - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 03-Dec-1999
 R;Tacke, R.; Boned, A.; Goridis, C.
 Nucleic Acids Res. 20, 5482, 1992
 A;Title: ASF alternative transcripts are highly conserved between mouse and man.
 A;Reference number: S26404
 A;Accession: S26404
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-201 <TCAC>
 A;Cross-references: EMBL:X66091
 A;Note: The nucleotide sequence was submitted to the EMBL Data Library, May 1992
 C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoproteins
 F;17-81/Domain: ribonucleoprotein repeat homology <RRM1>
 F;122-182/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 51 4%; Score 55; DB 2; Length 201;
 Best Local Similarity 55.0%; Pred. No. 18; Mismatches 9; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 RGRGAGAAARASGPGGGAP 20
 Db 90 RSGRGTGRGGGGGGGAP 109

RESULT 14
 A0040
 alternative splicing factor ASF-1 - human
 C;Species: Homo sapiens (man)
 C;Accession: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 21-Jul-2000
 R;Ge, H.; Zuo, P.; Manley, J.L.
 Cell 66, 373-382, 1991
 A;Title: Primary structure of the human splicing factor ASF reveals similarities with I
 A;Reference number: A40040; MUID:91309149; PMID:1855527
 A;Accession: A40040
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-248 <GEA>
 A;Cross-references: GB:MT2709; NID:9179073; PIDN:AAA35565.1; PMID:9179075
 R;Krainer, A.R.; Mayeda, A.; Rozak, D.; Birnstiel, M.; Binn, G.
 Cell 66, 383-394, 1991
 A;Title: Functional expression of cloned human splicing factor SF2: homology to RNA-bir
 A;Accession: B40041
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-248 <KRA>
 A;Cross-references: GB:M69040; NID:9338046; PIDN:AAA03476.1; PMID:9338047
 C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoproteins
 F;17-81/Domain: ribonucleoprotein repeat homology <RRM1>
 F;122-182/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 51 4%; Score 55; DB 2; Length 248;
 Best Local Similarity 55.0%; Pred. No. 21; Mismatches 9; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 RGRGAGAAARASGPGGGAP 20
 Db 90 RSGRGTGRGGGGGGGAP 109

RESULT 15

T46417 hypothetical protein DKFPZp434K1323.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46417
R;Blum, H.; Bauersachs, S.; Meves, H.W.; Gassendorfer, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z233034
A;Accession: T46417
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-250 <AAA>
A;Cross-references: BML:Al13714
A;Experimental source: adult testis; clone DKFPZp434K1323
C;Genetics:
A;Note: DKFPZp434K1323.1

Query Match Score 55; DB 2; Length 250;
Best Local Similarity 68.0%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 RGPGRGAGAAASGPGG 16
Db 9 RGERGGGAAALGPGG 24

Search completed: June 22, 2004, 08:54:02
Job time : 19 secs

PT DOMAIN 5 82 GLY-RICH.
 PT TRANSMEM 156 172 POTENTIAL. B122C5C28BR1569 CRC64;
 SQ SEQUENCE 180 AA; 17992 MW; B122C5C28BR1569 CRC64;

Query Match 100.0%; Score 107; DB 1; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2-pe-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Caps 0;

Qy 1 RGPRGAGAARASGPCCGAPR 20
 Db 43 RGPRGAGAARASGPCCGAPR 62

RESULT 2

CG2_HUMAN STANDARD; PRT; 210 AA.
 ID CTG2_HUMAN STANDARD; PRT; 210 AA.
 AC 075638; 075637; 39; Created
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cancer/testis antigen 2 (LAGE-1 protein).
 DE CTAG2 OR LAGE1.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
 OC NCBI TaxID=9606;
 OX RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3 (2) / ML45;
 RX MEDLINE=21986410; PubMed=12000953;
 RA Bentley S.D., Chater K.P., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabbinkowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hewitt D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3 (2)." [2]
 RN Nature 417:141-147 (2002).
 RP SEQUENCE OF 1-255 FROM N.A.
 RC STRAIN-A3 (2);
 RX MEDLINE=9405247; PubMed=8253693;
 RA Blanco G., Perez A., Brian P., Mendez C., Chater K.F., Salas J.A.;
 RT "A hydroxylase-like gene product contributes to synthesis of a
 polyketide spore pigment in Streptomyces halstedii." [3]
 PT polyketide
 RL J. Bacteriol. 175:8041-8048 (1993).
 CC -!- FUNCTION: Involved in developmentally regulated synthesis of a
 compound biosynthetically related to polyketide antibiotics which
 is essential for spore color in Streptococcus coelicolor.
 CC -!- COFACTOR: FAD (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE PHEA/TFDB FAMILY OF FAD MONOOXYGENASES.

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CC DR EMBL; AL939117; CAB45603; CAA52289; CAA52289.1; -.
 CC DR EMBL; X74213; CAA52289.1; -.
 CC DR EMBL; T35608; T35608; Collagen.
 CC DR InterPro; IPR008160; Collagen.
 CC DR InterPro; IPR000723; Flav_monoxygenase.
 CC DR InterPro; IPR002938; Moxy_FAD_Binding.
 CC DR InterPro; IPR003042; Rng_moxygenase.
 CC DR Pfam; PF01490; FAD_binding_3; 1.
 CC DR Pfam; PF01360; Monoxygenase; 1.

POLY-PRO.
 MSWDDPREGAGRMVVGIGLSASPEGGKARDLTPKHKV
 SQRPGTGPPEPGAQGDCRGAVFNWFSAPHI -> IR
 LTAADERQQLSSCLQQSLMLWITCPLPVFLAQASG
 QRR (in isoform LAGE-1A).
 /FTid=VP_004301.

FT VARIANT 6 6 R -> Q.
 FT VARIANT 89 89 E -> Q.
 FT /FTid=VAR_007855.
 FT /FTid=VAR_007856.

PRINTS: PRO0420; RINGMNOXGNASE.
 KW Oxidoreductase; Flavoprotein; FAD; Complete proteome.
 NP BIND 22 51 FAD (POTENTIAL).
 NP BIND 309 319 FAD (POTENTIAL).
 FT CONFLICT 60 60 R -> A (IN REF 2).
 FT CONFLICT 145 145 L -> LH (IN REF 2).
 FT CONFLICT 234 234 C -> S (IN REF 2).
 SQ SEQUENCE 627 AA; 64557 MW; 746B8AA2A9E9511C CRC64;

Query Match: Score 67; DB 1; Length 627;
 Best Local Similarity 75.0%; Pred. No. 1.7;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 GPRGAGAARASGPGG 17
 Db 447 GPRGAGAAGGGGGGG 462

RESULT 4
 CT86 HUMAN STANDARD PRT; 337 AA.
 AC Q9BZ19;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Hypothetical protein c20orf86.
 GN C20ORF86.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A.

- RX MEDLINE:21638749; PubMed:11780052;
 RA Deloukas P., Matthews L.H., Ashurst J.J., Burton J., Gilbert J.G.R.,
 Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baggaley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beirne D.M.,
 RA Beasley O.P., Bird C.P., Blakley S.B., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrell W.D., Butler A.P., Carter C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Cleo C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhaun P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Guilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaesaithai M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McElroy K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nicholson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillips B.J.C.T., Prathalingam S.R., Plumb R.W., Ramay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Yang-Beng T.L., Francke U.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wimling L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 CC -!- SIMILARITY: Contains 2 ANK repeats.
 CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.

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DR HSSP; P42771; 1DC2.
 DR Genew; HGNC:16117; C20orf86.
 DR InterPro; IPR02110; ANK.
 DR InterPro; IPR00626; Ubiquitin.
 DR PFAM; PF00023; ankyrin.
 DR SMART; SM00248; ANK_2.
 DR PRINTS; PRO1415; ANKININ.
 DR PROSITE; PS50088; ANK_REPEAT.
 DR PROSITE; PS50297; ANK_REPEAT_REGION_1.
 DR PROSITE; PS500299; UBIQUITIN_1; FALSE_NEG.
 DR PROSITE; PS500033; UBIQUITIN_2.
 DR PROSITE; PS500034; UBIQUITIN_2.
 DR PROSITE; PS500035; UBIQUITIN_REPEAT.
 DR PROSITE; PS500036; UBIQUITIN-LIKE.
 DR Hypothetical protein; ANK repeat; Polymorphism.
 DR DOMAIN 88 164 UBIQUITIN DOMAIN.
 FT REPEAT 211 241 ANK 1.
 FT REPEAT 244 273 ANK 2.
 FT VARIANT 287 287 R -> C (in dbSNP:584855).
 /FT IDVAR 014400.
 SQ SEQUENCE 337 AA; 36714 MW; EC8B4AAB41A4756CB CRC64;

Query Match: Score 64; DB 1; Length 337;
 Best Local Similarity 65.0%; Pred. No. 2;
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 RGPGRGAAARASGPCCAPR 20
 Db 3 RAAAGGGARRAAGPTGASR 22

RESULT 5
 A2AA_HUMAN STANDARD PRT; 450 AA.
 ID A2AA_HUMAN STANDARD PRT; 450 AA.
 AC P08913; Q9BZK1;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-2A adrenoreceptor (Alpha-2A adrenoreceptor) [Alpha-2A AR]
 DE ADRA2A OR ADRA2R OR ADRAR.
 GN Homo sapiens (Human).
 OS Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buterata; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A.
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE:89308571; PubMed:2568356;
 RA Fraser C.M., Arakawa S., McCombie W.R., Venter J.C.;
 RA Cloning, sequence analysis, and permanent expression of a human
 alpha-2-adrenergic receptor in Chinese hamster ovary cells. Evidence
 for independent pathways of receptor coupling to adenylylate cyclase
 RT attenuation and activation."
 RT J. Biol. Chem. 264:11754-11761 (1989).
 RN [2] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RN TISSUE=Platelet;
 RX MEDLINE:9042789; PubMed:2823383;
 RA Kobayashi B.K., Matsui H., Kobika T.S., Yang-Beng T.L., Francke U.,
 RA Carson M.G., Lefkowitz R.J., Regan J.W.;
 RA "Cloning, sequencing, and expression of the gene coding for the human
 alpha-2-adrenergic receptor. Allosteric modulation by Na+, H+, and
 RT amiloride analogs." J. Biol. Chem. 265:17307-17317 (1990).
 RN [4] SEQUENCE FROM N.A.
 RA Castellano M., Giacche M., Rossi F., Rivadossi P., Perani C.,
 RA Beschi M., Agabiti Rosei E.;

"A search for genetic variability in the human alpha-2 adrenergic receptor on chromosome 10." ; EMBL/GenBank/DBJ databases. [5] Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A., AND VARIANT LYS-251. DR GO; GO:0004938; P:alpha2-adrenergic receptor activity; TAS. DR GO; GO:0015559; P:potassium channel regulator activity; TAS. DR GO; GO:0030016; P:actin cytoskeleton regulation and biogenesis; TAS. DR GO; GO:0000387; P:activation of MAPK; TAS.

RP GO; GO:0006328; P:cell motility; TAS. DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. - ; TAS. DR GO; GO:0007394; P:negative regulation of adenylyl cyclase ac. - ; TAS. DR GO; GO:0008384; P:positive regulation of cell proliferation; TAS. DR GO; GO:0007265; P:RAS protein signal transduction; TAS. DR GO; GO:0007266; P:Rho protein signal transduction; TAS. DR GO; GO:0007165; P:signal transduction; TAS.

[6] DR InterPro; IPR00276; GPCR_Rhodopsin. DR Pfam; PF00001; rem1_1. DR PRINTS; PR00237; GPROTEIN_RECBP_F1_1. DR PROSITE; PS00237; G_PROTEIN_RECCEP_F2_1. DR PROSITE; PS0562; G_Protein_Coupled_Receptor_Transmembrane_Glycoprotein; KW Multigene family; Phosphorylation; Lipoprotein; Palmitate; KW Polymorphism; 3D-structure.

[7] DR DOMAIN; 1 33 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 34 59 CYTOPLASMIC (POTENTIAL). FT DOMAIN 60 70 1 (POTENTIAL). FT TRANSMEM 71 96 2 (POTENTIAL). FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 107 129 3 (POTENTIAL). FT DOMAIN 130 143 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 150 173 4 (POTENTIAL). FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 193 217 5 (POTENTIAL). FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 375 399 6 (POTENTIAL). FT DOMAIN 400 406 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 407 430 7 (POTENTIAL). FT DOMAIN 431 450 N-LINKED (GLCNAC. .) (POTENTIAL). FT CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).

[8] RP MUTAGENESIS OF PHE-412. DR DOMAIN; 14 14 (POTENTIAL). DR MEDLINE=9332079; PubMed=1678390; SURYANARAYANA S., Daunt D.A., von Zastrow M., Kobilka B.K.; "Human alpha-2A adrenergic receptor gene and the genotype of -1296 nucleotide and motionsickness." ; RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RT "A point mutation in the seventh hydrophobic domain of the alpha 2 adrenergic receptor increases its affinity for a family of beta adrenergic antagonists." ; RT J. Biol. Chem. 266:15488-15492 (1991). [9]

RP MUTAGENESIS OF ASPARTIC ACID AND SERINE RESIDUES. DR MEDLINE=91342598; PubMed=1678350; WANG C.-D., BACK M.A., FRASER C.M.; "Site-directed mutagenesis of alpha 2A-adrenergic receptors: identification of amino acids involved in ligand binding and receptor activation by agonists." ; RT Mol. Pharmacol. 40:168-179 (1991). DR "INDUCTION: Alpha-2 adrenergic receptors mediate the catecholamine-induced inhibition of adenylyl cyclase through the action of G proteins. The rank order of potency for agonists of this receptor is oxymetazoline > clonidine > epinephrine > norepinephrine > phenylephrine > dopamine > p-synephrine > p-tyramine > serotonin = p-octopamine. For antagonists the rank order is yohimbine > phentolamine = mianserin > chlorpromazine = spiperone = prazosin > drenanolol > alprenolol > pindolol." ; CC SUBCELLULAR LOCATION: Integral membrane protein. CC SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL; M23333; AAA5165_1; -.

CC DR EMBL; M1815; AAA5164_1; -.

CC DR EMBL; AF282016; AAGG0447_2; -.

CC DR EMBL; AP281308; AAF81441_1; -.

CC DR EMBL; AF316894; AAK01634_1; -.

CC DR EMBL; AF284095; AAK26743_1; -.

CC DR EMBL; AY012736; AAKS1162_1; -.

CC PIR; A34169; A34169. DR 1HHL; 10-APR-02. DR 1H09; 24-JUL-02. DR 1HOD; 24-JUL-02. DR 1HOP; 24-JUL-02. Genev; HGNC:281; ADD2A. DR MM; 104210; -.

CC GO; GO:0005887; C:integral to plasma membrane; TAS. DR GO; 00005887;

DR GO; GO:0004938; P:alpha2-adrenergic receptor activity; TAS. DR GO; GO:0015559; P:potassium channel regulator activity; TAS. DR GO; GO:0030016; P:actin cytoskeleton regulation and biogenesis; TAS. DR GO; GO:0000387; P:activation of MAPK; TAS.

RP GO; GO:0006328; P:cell motility; TAS. DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. - ; TAS. DR GO; GO:0007394; P:negative regulation of adenylyl cyclase ac. - ; TAS. DR GO; GO:0008384; P:positive regulation of cell proliferation; TAS. DR GO; GO:0007265; P:RAS protein signal transduction; TAS. DR GO; GO:0007266; P:Rho protein signal transduction; TAS. DR InterPro; IPR00276; GPCR_Rhodopsin. DR Pfam; PF00001; rem1_1. DR PRINTS; PR00237; GPROTEIN_RECBP_F1_1. DR PROSITE; PS00237; G_PROTEIN_RECCEP_F2_1. DR PROSITE; PS0562; G_Protein_Coupled_Receptor_Transmembrane_Glycoprotein; KW Multigene family; Phosphorylation; Lipoprotein; Palmitate; KW Polymorphism; 3D-structure.

FT DOMAIN; 1 33 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 34 59 CYTOPLASMIC (POTENTIAL). FT DOMAIN 60 70 1 (POTENTIAL). FT TRANSMEM 71 96 2 (POTENTIAL). FT DOMAIN 97 106 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 107 129 3 (POTENTIAL). FT DOMAIN 130 143 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 150 173 4 (POTENTIAL). FT DOMAIN 174 192 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 193 217 5 (POTENTIAL). FT DOMAIN 218 374 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 375 399 6 (POTENTIAL). FT DOMAIN 400 406 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 407 430 7 (POTENTIAL). FT DOMAIN 431 450 N-LINKED (GLCNAC. .) (POTENTIAL). FT CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).

FT DOMAIN; 14 14 (POTENTIAL). DR DOMAIN; 16 188 S-Palmitoyl cysteine (BY similarity). DR DISULFID 442 442 IMPLICATED IN LIGAND BINDING. DR LIPID 442 442 IMPLICATED IN CATECHOL AGONIST BINDING AND RECEPTOR ACTIVATION. DR FTID=VAR_014957. DR D->N: NO CHANGE IN BINDING AFFINITY. DR AND RECEPTOR ACTIVATION. DR BLIMINATES GUANINE NUCLEOTIDE-SENSITIVE AGONIST BINDING. DR N -> K (Rare polymorphism; frequency in Caucasians 0.004 and in African-Americans 0.05; 40% increase in agonist-promoted Gi coupling; dbSNP:1800035).

FT MUTAGEN 204 204 IMPLICATED IN CATECHOL AGONIST BINDING

FT VARIANT 251 251 IN ADENYLYL CYCLASE ACTIVITY.

FT MUTAGEN 113 113 D->N: LOWER AFFINITY FOR AGONISTS.

FT MUTAGEN 130 130 ELIMINATES GUANINE NUCLEOTIDE-SENSITIVE AGONIST BINDING.

FT MUTAGEN 200 200 S->A: LOWER AFFINITY FOR AGONISTS. NO CHANGE IN GUANINE NUCLEOTIDE-SENSITIVE AGONIST BINDING.

FT MUTAGEN 204 204 S->A: LOWER AFFINITY FOR AGONISTS.

FT MUTAGEN 79 79 REDUCED GUANINE NUCLEOTIDE-SENSITIVE AGONIST BINDING.

FT MUTAGEN 113 113 D->N: LOWER AFFINITY FOR AGONISTS.

FT MUTAGEN 130 130 ELIMINATES GUANINE NUCLEOTIDE-SENSITIVE AGONIST BINDING.

FT MUTAGEN 200 200 S->A: LOWER AFFINITY FOR BETA-ANTAGONIST ALPRENOLOL.

FT MUTAGEN 104 104 R -> T (IN REF. 2).

FT MUTAGEN 157 157 V -> C (IN REF. 2).

FT MUTAGEN 333 365 RGRPGATGTRGPAAGCBERGAAKASRMGRGR -> RGAG RCRRGSGTRGTRGQGRGASGLPERRAGGG (IN REF. 1 AND 2).

FT MUTAGEN 368 368 R -> L (IN REF. 2).

SO SEQUENCE 450 AA; 48956 MW; A703CP26204BBAC CRC64;

Query Match Similarity 56.1%; Score 60; DB 1; Length 450;
Best Local Similarity 63.6%; Pred. No. 7;
Matches 14; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

FT DOMAIN 69 498 GLY-RICH.
FT DOMAIN 499 613 ALA,GLY/PRO-RICH.
FT SEQUENCE 721 AA; 74226 MN; 482C7A765C603B4A CRC64;

Query 1 RGPRGAGAARAS-GPGGGAPR 20
Db 313 RGPRGKAKARASQVKEDSLPR 334

RESULT 6
PUB2 RAT STANDARD; PRT; 721 AA.

AC Q99PES;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DS Far upstream element binding protein 2 (FUSE binding protein 2) (KH type splicing regulatory protein) (KSFRP) (MAP2 RNA trans-acting protein 1); (MARTA).
DE FUBP2 OR KHSPP.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.
RN [1] - Taxid:10116;
RP SEQUENCE FROM N.A., SEQUENCE OF 73-87; 89-108 AND 475-486, SUBCELLULAR LOCATION, AND FUNCTION.
RP TISSUE=Brain;
RC MEDLINE=2246918; PubMed=12358951;
RA Rehbein M., Weger K., Duck P., Schweizer M., Richter D., Kindler S.;
RT "Molecular characterization of MARTA1, a protein interacting with the dendritic targeting element of MAP2 mRNAs.";
RL J. Neurochem. 82:1039-1046(2002).
.-!- FUNCTION: Part of a ternary complex that binds to the downstream control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in transcripts that are subject to tissue-specific alternative splicing. May interact with single-stranded DNA from the far-upstream element (FUSE). May activate gene expression (By similarity). Binds to the dendritic targeting element and may play a role in mRNA trafficking.
CC -!- SUBUNIT: Part of a ternary complex containing FUBP1, PRBP1, PTBP2 and HNRPH1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear. A small proportion is also found in the cytoplasm of neuronal cell bodies and dendrites.
CC -!- SIMILARITY: Contains 4 KH domains.

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CC CC Name=2;
CC IsoId=P54757-1; Sequence=VSP_003001;
CC IsoId=P54757-2; Sequence=VSP_003001;
CC Name=3;
CC IsoId=P54757-3; Sequence=VSP_003002;
CC Name=4;
CC IsoId=P54757-4; Sequence=VSP_003002; VSP_003003;
CC Name=5;
CC IsoId=P54757-5; Sequence=VSP_003001, VSP_003002;
CC Name=6;
CC IsoId=P54757-6; Sequence=VSP_003000, VSP_003002;
CC -!- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.

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CC DR IM308818; AAC39811.1; -.
CC DR InterPro; IPR004087; KH_dom.
CC DR InterPro; IPR04088; KH_type_1.
CC DR SMART; SM00322; KH; 4.
CC DR PROSITE; PS5004; KH_TYPE_1; 4.
CC KW Transport; mRNA transport; mRNA processing; mRNA splicing;
CC KW Transcription regulation; Trans-acting factor; Nuclear protein;
CC KW DNA-binding; RNA-binding; Repeat.
CC FT DOMAIN 145 209 KH 1.
CC FT DOMAIN 234 300 KH 2.
CC FT DOMAIN 323 387 KH 3.
CC FT DOMAIN 425 492 KH 4.
CC FT DOMAIN 572 685 4 X 12 AA IMPERFECT REPEATS.
CC FT REPEAT 572 583 1.
CC FT REPEAT 618 629 2.
CC FT REPEAT 644 655 3.
CC FT DOMAIN 674 685 4.
CC FT DOMAIN 7 685 4.
CC GLY/PRO-RICH.

RESULT 7
PUB5 RAT STANDARD; PRT; 1005 AA.

AC P54757;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EHK-1) (EPH homology kinase-1).
DB EPHAS OR EHK1 OR EHK-1.
GN Rattus norvegicus (Rat).
OS Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
OX RN [1];
RN RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
RN RP SEQUENCE FROM N.A. (ISOFORM 6).
RN STRAIN=Sprague-Dawley; TISSUE=Brain;
RN MEDLINE=9406777; PubMed=7504232;
RN Maisonnierre P. C., Barrezueta N.X., Yancopoulos G.D.;
RN RT "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with different structures and neuronal expression.";
RN RT Oncogene 8:3277-3288 (1993).
RN [2].
RN RP SEQUENCE FROM N.A. (ISOFORM 6).
RN RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RN MEDLINE=95205646; PubMed=7838646;
RN RA Taylor V., Miescher G.C., Pfearr S., Honegger P., Breitschopf H.,
RN RA Lassmann H., Steck A.J.;
RN RT "Expression and developmental regulation of Ehk-1, a neuronal Elk-like receptor tyrosine kinase in brain.";
RN RL Neuroscience 63:163-178 (1994).
RN CC -!- FUNCTION: Receptor for members of the ephrin-A family. Binds to ephrin-A1, -A2, -A3, -A4 and -A5.
RN CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
RN CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
RN CC -!- ALTERNATIVE PRODUCTS:
RN CC Event=Alternative splicing; Named isoforms=6;
RN CC Name=1;
RN CC IsoId=D54757-1; Sequence=Displayed;
RN CC Name=2;
RN CC IsoId=P54757-2; Sequence=VSP_003001;
RN CC Name=3;
RN CC IsoId=P54757-3; Sequence=VSP_003002;
RN CC Name=4;
RN CC IsoId=P54757-4; Sequence=VSP_003002; VSP_003003;
RN CC Name=5;
RN CC IsoId=P54757-5; Sequence=VSP_003001, VSP_003002;
RN CC Name=6;
RN CC IsoId=P54757-6; Sequence=VSP_003000, VSP_003002;
RN CC -!- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
RN CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
RN CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
RN CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.

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CC	EMBL; X78689; CAA53257.1; -.	FT	
CC	PIR; S49015; S49015.	FT	
CC	DR; S51603; S51603.	FT	
CC	HSSP; PD0523; PTK.	FT	
CC	DR; InterPro; IPR006209; EGFR like.	FT	
CC	DR; InterPro; IPR001030; Ephrin receptor.	FT	
CC	DR; InterPro; IPR009857; FN III-like.	FT	
CC	DR; InterPro; IPR003962; FNIII subd.	FT	
CC	DR; InterPro; IPR008979; Gal bind like.	FT	
CC	DR; InterPro; IPR000719; Proc_kinase.	FT	
CC	DR; InterPro; IPR001660; SAM.	FT	
CC	DR; InterPro; IPR001245; Tyr_Ptknase.	FT	
CC	DR; InterPro; IPR001566; Tyr_Pkinase_AS.	FT	
CC	DR; InterPro; IPR001426; Ykase_receptor.	FT	
CC	PFam; PF001404; EPH_1b.	FT	
CC	PFam; PF00041; fn3_2.	FT	
CC	PFam; PF00069; kinase.	FT	
CC	DR; PFam; PF00536; SAM; 1.	FT	
CC	PRINTS; PR00014; FNTYPEBLLI.	FT	
CC	PRINTS; PR00109; TYRKINASE.	FT	
CC	PRODOM; PD001495; Ephrin receptor; 1.	FT	
CC	SMART; SM00615; EPH_1b; 1.	FT	
CC	SMART; SM00060; FN1; 2.	FT	
CC	DR; PROSITE; PS00219; T-YKCK; 1.	FT	
CC	DR; PROSITE; PS00186; EGP_2; UNKNOWN_1.	FT	
CC	DR; PROSITE; PS00001; PROTEIN_KINASE_ATP; FALSE_NEG.	FT	
CC	DR; PROSITE; PS00010; PROTEIN_KINASE_DOM; 1.	FT	
CC	DR; PROSITE; PS00019; PROTEIN_KINASE_TYR; 1.	FT	
CC	DR; PROSITE; PS00790; RECEPTOR_TTR_KIN_V_1; 1.	FT	
CC	DR; PROSITE; PS00791; RECEPTOR_TTR_KIN_V_2; 1.	FT	
CC	DR; PROSITE; PS550105; SAM_DOMAIN; 1.	FT	
KW	Transfase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;	FT	
KW	Receptor; Transmembrane; Glycoprotein; Signal; Repeat;	FT	
KW	Alternative splicing.	FT	
FT	SIGNAL; 1	BY SIMILARITY.	FT
FT	CHAIN	EPHRIN TYPE-A RECEPTOR 5.	FT
FT	DOMAIN	EXTRACELLULAR (POTENTIAL).	FT
FT	TRANSMEM	POTENTIAL.	FT
FT	DOMAIN	CYTOSOLIC (POTENTIAL).	FT
FT	DOMAIN	CYS-RICH.	FT
FT	DOMAIN	FIBRONECTIN_TYPE-III_1.	FT
FT	DOMAIN	FIBRONECTIN_TYPE-III_2.	FT
FT	DOMAIN	PROTEIN KINASE.	FT
FT	DOMAIN	SAM.	FT
FT	NP_BIND	ATP (BY SIMILARITY).	FT
FT	BINDING	ATP (BY SIMILARITY).	FT
FT	ACT_SITE	BY SIMILARITY.	FT
FT	MOD_RES	PHOSPHORYLATION (AUTOMATIC).	FT
FT	MOD_RES	PHOSPHORYLATION (AUTOMATIC).	FT
FT	MOD_RES	PHOSPHORYLATION (AUTOMATIC).	FT
FT	MOD_RES	PHOSPHORYLATION (AUTOMATIC).	FT
FT	CARBODY	PHOSPHORYLATION (AUTOMATIC).	FT
FT	CARBODY	N-LINKED (GLCNAC). (POTENTIAL).	FT
FT	CARBODY	N-LINKED (GLCNAC). (POTENTIAL).	FT
FT	CARBODY	N-LINKED (GLCNAC). (POTENTIAL).	FT
FT	CARBODY	N-LINKED (GLCNAC). (POTENTIAL).	FT
FT	CARBODY	N-LINKED (GLCNAC). (POTENTIAL).	FT
FT	CARBODY	N-LINKED (GLCNAC). (POTENTIAL).	FT
FT	VARSPLIC	GRRETOGREGG > DADOPRAQASWCHARR (in isoform 6).	FT
FT	VARSPLIC	/PTID=VSP_003000.	FT
FT	VARSPLIC	VCPREPERKSPHSCTCSPCPHSYTHEBASTSCVCEXDYFR RESD8PTMACT -> G (in isoform 2 and isoform 5).	FT
FT	VARSPLIC	/PTID=VSP_003001.	FT
FT	VARSPLIC	RPPSPRNITSNNYNETSFLIEWIPPADTGGKDVSYYLCK RCNSHAGVIEEGGHVRYDPQIQIGLANTSVMNADPLHETNY	FT
FT	VARSPLIC	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,	RA

RA Schein J.E., Jones S.J.M., Marra M.A.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
PROC. NATL. ACAD. SCI. U.S.A. 99:16899-16903 (2002).
[4]

SEQUENCE OF 32-44.
TISSUE=Liver;

RX MEDLINE=94147969; PubMed=3133870;

RA Hughes G.J., Prutiger S., Paquet N., Pasquali C., Sanchez J.-C.,

Tissot J.-D., Barich A., Apel R.D., Hochstrasser D.F.;

RT Human liver protein map: update 1993. *;

Electrophoresis 14:1216-1222(1993).

-!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.

-!- CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.

-!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

-!- SIMILARITY: Belongs to the cytochrome c oxidase IVb family.

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CC EMBL: M59220; PDB52060.1;
DR EMBL; M19961; AA52061.1; -.

DR BC005229; AAH06229.1; -.

DR PIR: J70324; OMIM5B

DR PROSITE: PS00848; COXSB; 1.

DR PROSITE: PS00848; COXSB; 1.

KW Oxidoreductase; Inner membrane; Mitochondrion; Transit peptide;

KW TNCIT

FT TRANSIT 31 MITOCHONDRION.

FT CHAIN 32 129 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

SQ SEQUENCE 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

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FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

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FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

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FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

FT TNCIT 31 CYTOCHROME C OXIDASE POLYPEPTIDE VB.

FT METAL 91 91 ZINC (POTENTIAL).

FT METAL 113 113 ZINC (POTENTIAL).

FT METAL 116 116 ZINC (POTENTIAL).

FT CONFLICT 109 109 Q -> P (IN SEF. 1).

FT SEQ 129 AA; 8778F4CD34AC931 CRC64;

EPHRIN TYPE-A RECEPTOR 5.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 PT DOMAIN 27 412
 PT TRANSMEM 413 433
 PT DOMAIN 434 399
 PT DOMAIN 306 775
 PT DOMAIN 514 868
 PT DOMAIN 804 875
 PT SITE 875 875
 PT NP BIND 520 528
 PT BINDING 546 546
 PT ACT SITE 639 639
 PT MOD RES 489 495
 PT MOD RES 495 672
 PT MOD RES 672 821
 PT CARBOHYD 266 301
 PT CARBOHYD 301 877 AA;
 SEQUENCE 54AD2DCB64178214 CRC64;
 MW: 97115 MW;

Query Match
 Best Local Similarity 55.1%; Score 59; DB 1; Length 877;
 Matches 13; Conservative 0; Nsmatches 6; Indels 2; Gaps 1;

Qy	2 GPRGCAARRASGPGCC- APR 20
Db	5 GPRGAGHRRTQQGCCDDPR 25

RESULT 10
COXB_PAT STANDARD; PRT; 129 AA.
 ID _COXB_PAT STANDARD; PRT; 129 AA.
 AC P12015;
 DT 01-OCT-1989 [Rel. 12; Created]
 DT 01-FEB-1996 [Rel. 33; Last sequence update]
 DT 30-MAY-2000 [Rel. 39; Last annotation update]
 COX5B, Cytochrome C oxidase polypeptide Vb, mitochondrial precursor
 DE (EC 1.9.3.1) (VIA*).

OS Rattus norvegicus (Rat). Chordata; Craniata; Vertebrata; Euteleostomi; OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID:10116;
 RN [1] _
 RP STRAIN=Sprague-Dawley; TISSUE=Liver;
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 MEDLINE=94266742; PubMed=8206667;
 RA Goto Y., Amuro N., Okazaki T.;
 RT "Nucleotide sequence of cDNA for rat liver and brain cytochrome c
 oxidase subunit Vb." /
 RT Molecular cloning and characterization of the rat cytochrome c
 oxidase subunit Vb gene." /
 J. Biochem. 115:194-201(1994).
 RN [2]
 RP SEQUENCE OF 13-129 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 MEDLINE=89366666; PubMed=2549512;
 RA Goto Y., Amuro N., Okazaki T.;
 RT "Nucleotide sequence of cDNA for rat liver and brain cytochrome c
 oxidase subunit Vb." /
 RN Nucleic Acids Res. 17:6388-6398(1989).
 RN [3]
 RP SEQUENCE OF 32-41.
 RX MEDLINE=953224529; PubMed=1601105;
 RX STRAIN=Wistar; TISSUE=Liver;
 RA Schaegger H., Noack H., Falanek W., Brandt U., von Jagow G.;
 RT Cytochrome-c oxidase in developing rat heart. Enzymic properties and
 amino-terminal sequences suggest identity of the fetal heart and the
 adult liver isoform";
 RT Eur. J. Biochem. 30:235-241(1995).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
 chains of cytochrome c oxidase, the terminal oxidase in
 mitochondrial electron transport. It is a ferricytochrome
 CC -!- CATALYTIC ACTIVITY: 4 ferricytochrome c + O₂ = 4 ferricytochrome
 CC C + 2 H₂O. LOCATION: Mitochondrial inner membrane.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

RESULT 11
SRC2_HUMAN STANDARD; PRT; 870 AA.
 ID SRC2_HUMAN STANDARD;
 AC Q96GP6; Q9BW74;
 DT 28-FEB-2003 (Rel. 41; Created)
 DT 28-FEB-2003 (Rel. 41; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DB Scavenger receptor class F member 2 precursor (Scavenger receptor
 expressed by endothelial cells 2 protein) (SREC-II).
 GN SCAF2P OR SREC-II.
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Macromilia; Bilateria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=2267235; PubMed=12154095;
 RA Ishii J., Adachi H., Aoki J., Koizumi H., Tomita S., Suzuki T.,
 RA Tsujimoto M., Inoue K., Arai H.;
 RA "SREC-II, a new member of the scavenger receptor type F family,
 RT trans-interacts with SREC-I through its extracellular domain." /
 RT J. Biol. Chem. 277:39696-39702(2002).
 RN [2]
 RP SEQUENCE OF 272-870 FROM N.A., AND VARIANTS GLU-777 AND LEU-778.
 RX TISSUE=Brain;
 RX MEDLINE=22383257; PubMed=12477932;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Schuler G.D., Shemmen C.M., Wagner L., Schaefer C.F., Bhat N.R.,
 RA Altchul S.F., Zeeberg B., Buetow K.K., Schaefer C.F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabler M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA
 Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., RA
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA
 Rodriguez A.C., Grinberg J., Myers R.M., RA
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA
 Schnberk A., Schein J.E., Jones S.U.M., Marra M.A., RA
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences"; RA
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL CC -!- FUNCTION: Probable adhesion protein, which mediates homophilic and heterophilic interactions. In contrast to SCARF1, it poorly mediates the binding and degradation of acetylated low density lipoprotein (Ac-LDL) (By similarity).
 CC -!- SUBUNIT: Homophilic and heterophilic interaction via its extracellular domain. Interacts with SCARF1. The heterophilic interaction with SCARF1, which is stronger than the homophilic interaction with itself, is suppressed by the presence of SCARF1 ligand such as Ac-LDL (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE_SPECIFICITY: Predominantly expressed in endothelial cells. Expressed in heart, placenta, lung, kidney, spleen, small intestine and ovary.
 CC -!- SIMILARITY: Contains 7 EGF-like domains.
 CC -!- CAUTION: Ref 2 sequences differ from that shown due to frame-shifts in positions 750, 751 and 768.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR AF522196; AAN4861; -;
 DR EMBL; BC000594; AAH00594.1; ALT_FRAME.
 DR EMBL; BC009326; AAH09326.1; ALT_FRAME.
 DR Genew; HGNC:19869; SCARF2.
 DR InterPro; IPR006269; EGP_LIKE.
 DR InterPro; IPR006210; IEGF.
 DR PRINTS; PR00011; EGFLAMININ.
 DR SMART; SM00181; EGF; 7.
 DR SMART; SM00180; EGF_Lam; 6.
 DR PROSITE; PS000022; EGF_1; 7.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS05026; EGF_3; 3.
 DR Cell adhesion; Receptor; Repeat; Signal; Transmembrane; B
 KW BGF-like domain; Glycoprotein; Polymorphism.
 FT SIGNAL 1 43 SCAVENGER; RECEPTOR CLASS F MEMBER 2.
 FT CHAIN 44 870 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 44 441 442 462 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 442 462 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 463 830 831 CYTOSOLIC (POTENTIAL).
 FT DOMAIN 76 110 111 EGF-LIKE 1.
 FT DOMAIN 122 153 154 EGF-LIKE 2.
 FT DOMAIN 154 182 183 EGF-LIKE 3.
 FT DOMAIN 183 212 213 EGF-LIKE 4.
 FT DOMAIN 213 241 242 EGF-LIKE 5.
 FT DOMAIN 242 270 271 EGF-LIKE 6.
 FT DOMAIN 372 403 404 EGF-LIKE 7.
 FT DOMAIN 652 851 852 PRO-RICH.
 FT DISULFID 80 92 93 POTENTIAL.
 FT DISULFID 86 98 99 POTENTIAL.
 FT DISULFID 100 109 110 POTENTIAL.
 FT DISULFID 126 134 135 POTENTIAL.
 FT DISULFID 128 141 142 POTENTIAL.
 FT DISULFID 143 152 153 POTENTIAL.
 FT DISULFID 156 163 164 POTENTIAL.
 FT DISULFID 158 170 171 POTENTIAL.
 FT DISULFID 181 182 183 POTENTIAL.

POTENTIAL.
 PT DISULFID 185 193 POTENTIAL.
 PT DISULFID 187 200 POTENTIAL.
 PT DISULFID 202 211 POTENTIAL.
 PT DISULFID 215 222 POTENTIAL.
 PT DISULFID 217 229 POTENTIAL.
 PT DISULFID 231 240 POTENTIAL.
 PT DISULFID 244 251 POTENTIAL.
 PT DISULFID 246 258 N-LINKED (GLCNAC, . .) (POTENTIAL).
 PT DISULFID 260 269 N-LINKED (GLCNAC, . .) (POTENTIAL).
 PT DISULFID 376 384 N-LINKED (GLCNAC, . .) (POTENTIAL).
 PT DISULFID 379 391 N-LINKED (GLCNAC, . .) (POTENTIAL).
 PT DISULFID 393 402 /FTId=VAR 015148
 PT CARBOHYD 83 83 /FTId=VAR 015149
 PT CARBOHYD 310 315 /FTId=VAR 015150
 PT CARBOHYD 365 365 /FTId=VAR 015151
 PT VARIANT 403 403 /FTId=VAR 015151
 PT VARIANT 777 777 MISSING (TN REF 2).
 V-> L (IN dbSNP:759612).
 /FTId=VAR 015149
 A-> G (IN dbSNP:874100).
 /FTId=VAR 015150
 A-> G (IN dbSNP:874101).
 /FTId=VAR 015151
 REF 2; AAH00584).
 SQ SEQUENCE 870 AA; 92479 MW; DCB735A50E6B3D1P CRC64;
 Query Match 53.3%; Score 57; DB 1; Length 870;
 Best Local Similarity 73.3%; Pred. No. 26;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 12
 RLDB_XANAC STANDARD; PRT; 550 AA.
 ID RLDB_XANAC
 AC Q8PK58;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DB Ribosoma1 large subunit Pseudouridine Synthase B (EC 4.2.1.70)
 DE (Psuedouridylate synthase) (uracil hydrolyase).
 GN RLDB OR XAC21B
 OC Xanthomonas axonopodis (fp. citri).
 OC Bacteria: Proteobacteria: Gammaproteobacteria: Xanthomonadales:
 OC Xanthomonadaceae: Xanthomonas.
 RN [1] NCBI_TaxID=92899;
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=240215; PubMed=12024217;
 RA da Silva A.M., Kishii L.T., Leite R.P., Reinach F.C., Parach C.S., Purlan L.R., RA Katayama A.M., Kishii L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., RA Monteiro-Vitorelio C.B., Van Sluys M.A., Almeida N.F., RA Quaggio R.B., Monteiro-Vitorelio C.B., Van Sluys M.A., Madeira A.M.B.N., Martinez B.C., RA Alves L.M.C., do Amaral A.M., Bercolini M.C., Camargo L.F.A., RA Cardozo J.J., Chambergo S., Camaraote G., Cannavan F., Cardozo J.J., Chambergo S., RA Moreira L.M., Novo M.T.M., Oliveira M.C., Oliveira V.R., RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., RA Pereira H.A., Rossi A., Sena J.A.D., Salva C., de Souza R.F., RA Paria J.B., Pereira A.J.S., Ferreira R.C.C., Ferro M.I.T., RA Formighieri E.F., Franco M.C., Gregorio C.C., Gruber A., RA Katsuyama A.M., Kishii L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez B.C., RA Martins E.C., Meidanis J., Manch C.P.M., Miyaki C.Y., Moon D.H., RA Moreira L.M., Novo M.T.M., Oliveira M.C., Oliveira V.R., RA Pereira H.A., Rossi A., Sena J.A.D., Salva C., de Souza R.F., RA Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D., RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.P., RA Setubal J.C., Kitajima J.P.; RA
 RT Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.; RT

- RL Nature 417:459-463 (2002).
 CC -|- FUNCTION: Responsible for synthesis of pseudouridine from
 CC uracil-2'65 in 23S ribosomal RNA (By similarity).
 CC -|- CATALYTIC ACTIVITY: Uracil + D-ribose 5'-phosphate = pseudouridine
 CC 5'-phosphate + H(2)O.
 CC -|- SIMILARITY: Belongs to the pseudouridine synthase rsuA family.
 CC -|- SIMILARITY: Contains 1 S4 RNA-binding domain.
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- CC EMBL; AE011869; AAH37171.1;
 DR InterPro; IPR006145; Pseudour synth.
 DR InterPro; IPR000748; Psi_synth_RSU.
 DR InterPro; IPR004242; S4.
 PFam; PF06849; Pseudour synth_2; 1.
 PFam; PF01479; S4_1.
 TIGR3MS; TIGR0093; TIGR0093; 1.
 DR PROSITE; PS01119; PSI_RSU; 1.
 DR PROSITE; PS50889; S4_1.
 KW RNA processing; Lysate; RNA-binding; Complete proteome.
 FT DOMAIN 28 97 SA RNA-binding.
 FT ACT SITE 132 132 BY SIMILARITY.
 SQ SEQUENCE 550 AA; 57729 MW; 549B3A448C8C0A2 CRC64;
 Query Match 51.9%; Score 55.5%; DB 1; Length 550;
 Best Local Similarity 61.9%; Pred. No. 25;
 Matches 13; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
- Qy 1 RGPRG-AGARASPGPGGAPR 20
 Db 508 RGGGGPGGAGRPGGGAPR 528
- RESULT 13
 SPRI HUMAN STANDARD; PRT; 247 AA.
 ID Q07955; Q13809; PRT; 247 AA.
 AC Q07955; Q13809; PRT; 247 AA.
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-MAR-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DB Splicing factor; arginine-serine-rich 1 (pre-mRNA splicing factor SF2, P33 subunit) (AF SP2P33 OR ASF OR SF2).
 GN SFRS1 OR SF2P33 OR ASF OR SF2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID=9606;
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 143-160 AND 166-174.
 RX MEDLINE=91109150; PubMed=1830244;
 RA Krainer A.R.; Mayeda A.; Kozak D.; Binnis G;
 RT "Primary structure of the human splicing factor SF2: homology to RNA-binding proteins, u1 70K, and Drosophila splicing regulators,"; RT Cell 66:385-394 (1991).
 RL [1]
 RN SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND ALTERNATIVE SPLICING.
 RX MEDLINE=91109119; PubMed=1855557;
 RA Ge H.; Zuo P.; Manley J.L.; Binnis G;
 RT "Functional expression of cloned human splicing factor SF2 reveals similarities with Drosophila regulators,"; RT Cell 66:373-382 (1991).
 RL [2]
 RN SEQUENCE FROM N.A. (ISOFORM ASF-1).
 RX MEDLINE=22188257; PubMed=12477932;
 RA Straetling W.; Bourquin J.-P.; Stagljar I.; Lindemann L.; Jasper H.; Hartmann A.M.; Packelmeier F.O.; Ulrich A.; Stamm S.; RT "SAP-B couples transcription and pre-mRNA splicing to SAP/MAR
- RA Klausner R.D.; Collins F.S.; Wagner L.; Shemmen C.M.; Schuler G.D.; Aitschba S.F.; Zeerberg B.; Buetow K.H.; Schaeterle C.F.; Bhat N.K.; Hopkins R.P.; Jordan H.; Moore T.; Max S.I.; Wang J.; Biehl F.; Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.; Stepleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.B.; Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.; Raha S.S.; Loqueland N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.; Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Guarante P.H.; Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Rulyk S.W.; Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.; Farley J.; Heitz B.; Ketteman M.; Madan A.; Rodriguez S.; Sanchez A.; Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.; Blakesley R.W.; Touchman J.W.; Green B.D.; Dickson M.C.; Rodrigues A.C.; Grimes J.; Schmitz J.; Myers R.M.; Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.B.; Scheiner A.; Schein J.E.; Jones J.M.; Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences,"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
- [4] "SR proteins: a conserved family of pre-mRNA splicing factors."; Prok. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
- RN SEQUENCE OF 122-139.
 RX MEDLINE=92249775; PubMed=1577277;
 RA Zahler A.M.; Lane W.S.; Stolk J.A.; Roth M.B.; PT RT Genes Dev. 6:837-847 (1992).
- [5] INTERACTIONS IN SPLENOCYOME ASSEMBLY.
 RN MEDLINE=94084782; PubMed=8261505;
 RX MEDLINE=94187841; PubMed=8139654;
 RA Wu J.Y.; Maniatis T.; RA Kohitz J.D.; Jamison S.F.; Will C.L.; Zuo P.; Luhmann R.; PT RT "Specific interactions between proteins implicated in splice site selection and regulated alternative splicing."; Cell 75:1061-1070 (1993).
- [6] FUNCTION IN RECRUITMENT OF U1-70K TO PRE-mRNA.
 RN MEDLINE=94187841; PubMed=8139654;
 RX MEDLINE=94084782; PubMed=8261505;
 RA Garcia-Blanco M.A.; Manley J.L.; Zuo P.; Luhmann R.; PT RT "Protein-protein interactions and 5'-splice-site recognition in mammalian mRNA precursors."; Nature 368:119-124 (1994).
- [7] RNA BINDING SPECIFICITY.
 RX MEDLINE=95354672; PubMed=7543047;
 RA Tacke R.; Manley J.L.; RT RT "The human splicing factors ASF/SF2 and SC35 possess distinct, functionally significant RNA binding specificities."; EMBO J. 14:3540-3551 (1995).
- [8] MUTAGENESIS, AND CHARACTERIZATION OF FUNCTIONAL DOMAINS.
 RX MEDLINE=94039556; PubMed=8223481;
 RA Zuo P.; Manley J.L.; RA "Functional domains of the human splicing factor ASF/SF2."; RT RT EMBO J. 12:4727-4737 (1993).
 RL [9]
 RN RECOGNITION OF PRE-mRNA 5'-SPLICE SITES.
 RX MEDLINE=94211864; PubMed=7512732;
 RA Mayeda A.; Zahler A.M.; Krainer A.R.; Roth M.B.; RT RT "Two members of a conserved family of nuclear phosphoproteins are involved in pre-mRNA splicing.";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:1301-1304 (1992).
 RL [10]
 RN CHARACTERIZATION.
 RX MEDLINE=92159037; PubMed=1741384;
 RA Mayeda A.; Zahler A.M.; Krainer A.R.; Roth M.B.; RT RT "Two members of a conserved family of nuclear phosphoproteins are involved in pre-mRNA splicing.";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:1301-1304 (1992).
 RL [11]
 RN INTERACTION WITH SAPB/SAPB1.
 RX MEDLINE=98337913; PubMed=9671816;
 RA Mayer O.; Straetling W.; Bourquin J.-P.; Stagljar I.; Lindemann L.; Jasper H.; Hartmann A.M.; Packelmeier F.O.; Ulrich A.; Stamm S.; RT "SAP-B couples transcription and pre-mRNA splicing to SAP/MAR

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CC RX MEDLINE=94018466; PubMed=8412494;
 CC RA Blaxall H.S.; Heck D.A.; Bylund D.B.;
 CC RT "Molecular determinants of the alpha-2D adrenergic receptor subtype.";
 CC PL Life Sci 53:9-9 (1993).
 CC -!- FUNCTION: Alpha-2 adrenergic receptors mediate the catecholamine-induced inhibition of adenylyl cyclase through the action of G proteins.
 CC SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SUBCELLULAR SPECIFICITY: Retina, brain and olfactory lobe.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions is long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AF005031; BAC70762.1; -.
 DR HAMAP: MF_00100; -!- 1.
 DR InterPro: IPR001851; Bac_immem_transp.
 DR InterPro: IPR004161; BFM_immem.
 DR InterPro: IPR004161; BFM_D2.
 DR InterPro: IPR003577; BP_GTPbind.
 DR InterPro: IPR003577; GTPBase_Ras.
 DR InterPro: IPR00118; IP2.
 DR InterPro: IPR006847; IP2_N.
 DR InterPro: IPR002965; Prich_extensn.
 DR InterPro: IPR01806; Ras_transfing.
 DR InterPro: IPR005225; Small_GTP.
 DR InterPro: IPR009000; Translat_Factor.
 PFam: PF00009; GTP_EFTU; 1.
 PFam: PF03144; GTP_EFTU_D2; 1.
 DR PRINTS: PRO0315; ELONGATINFFECT.
 DR PRINTS: PRO1217; RICHAXTEINS.
 DR PRINTS: PRO0049; RASTERSPRNG.
 PRODom: PD186100; IPF2; 1.
 SMART: SM00171; RAS; 1.
 TIGRFAMS: TIGR00487; IP-2; 1.
 DR TIGRFAMS: TIGR00231; small_GTP; 1.
 DR PROSITE: PS00176; IPF2; PALES_NEG.
 DR Initiation_factor; Protein biosynthesis; GTP-binding.
 KW Complete proteome.
 KW G-DOMAIN
 FT DOMAIN 542 694 GTP (BY SIMILARITY).
 NP_BIND 548 555 GTP (BY SIMILARITY).
 FT NP_BIND 598 602 GTP (BY SIMILARITY).
 FT NP_BIND 652 655 GTP (BY SIMILARITY).
 SQ SEQUENCE 1046 AA; 106882 MW; 62B12E2DPAA55 CRC64;
 Query Match 51.4%; Score 55; DB 1; Length 1046;
 Best Local Similarity 60.0%; Pred. No. 50;
 Matches 12; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
 Qy 1 RGPGAGAGARAAGGGGAGR 20
 Db 328 RGPGGGG--RGPGGGGGGR 345
 RESULT 15
 A2AA_BOVIN STANDARD; PRT; 452 AA.
 ID A2AA_BOVIN
 AC Q28738;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-2A adrenergic receptor (Alpha-2A adrenoreceptor) (Alpha-2AR)
 DE (Alpha-2D adrenergic receptor) (Alpha-2AR).
 GN ADRA2A.
 OS Bos taurus (Bovine).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=98111113; PubMed=9450652;
 RX Perna_V.; Duda_T.; Sharma_R.K.; Venkateswaran_Y.;
 RT "The bovine alpha-2D-adrenergic receptor gene: structure, expression
 RT in retina, and pharmacological characterization of the encoded
 RT receptor";
 RL Mol. Cell. Biochem. 177:113-123 (1997).
 RN [2] SEQUENCE OF 171-210 FROM N.A.

Search completed: June 22, 2004, 08:51:57
 Job time : 16 secs

GenCore - protein search, using sw model

Run on: June 22, 2004, 08:47:17 ; Search time 48 Seconds
(without alignments)
131.466 Million cell updates/sec

Title: US-09-529-206D-4_COPY_43_62

Effect score: 1 RGPGRGAAARASPGGGAPR 20

Querence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Search space: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25; *

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_wbc:*

B: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriaph:*

17: sp_archeap:*

RESULTS

RESULT 1

ID Q9NY13 PRELIMINARY;

AC Q9NY13;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Hypothetical protein (Fragment).

GN LAGE2.

OS Homo sapiens (Human)

OC Bukayoya; Metzoco; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI-TaxId=9606;

RN [1] -

RP SEQUENCEB FROM N.A.

RA Lettre B.G.;

RL Submitted (MAR-2000) to the ENSEMBL/GenBank/DDBJ databases.

DR EMBL: AJ273978; CAB6945; 1. - .

KW Hypothetical protein.

FT NON_TTR 1 1

SEQUENCE 142 AA; 13895 MW; 2788E922AC4ACC7B CRC64;

SQ Query Match Length DB ID Description

1 107 100.0 142 09ny13 09ny13 homo sapien

2 99 92.5 180 4 Q9Y479 09y479 homo sapien

3 99 92.5 210 4 Q9BU80 Q9BU80 homo sapien

4 99 92.5 210 4 Q9UJB9 Q9ujb9 homo sapien

5 62 57.9 301 5 Q8WSZ3 Q8wsz3 nephila clavipes

6 62 57.9 550 5 Q86Z11 Q86z11 toxoplasma

7 62 57.9 1039 10 Q8S0W4 Q8sw04 oryza sativa

8 61.5 57.5 1953 5 Q9BIT7 Q9bit7 nephila ina

9 60 56.1 465 4 Q86TH8 Q86th8 homo sapien

10 60 56.1 926 11 Q8R554 Q8r554 mus musculus

11 59 55.1 420 11 Q8CXY9 Q8cxy9 mus musculus

12 59 55.1 538 11 Q8C278 Q8c278 mus musculus

13 59 55.1 681 11 Q8C276 Q8c276 mus musculus

14 58.5 54.7 563 5 Q9BITS5 Q9bits5 nephila ina

15 58.5 54.7 566 5 Q19581 Q19581 caenorhabditis elegans

16 58.5 54.7 569 5 Q9C522 Q9c522 caenorhabditis elegans

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query	Match	Length	DB	ID	Description
1	107	100.0	142	4	09ny13	09ny13 homo sapien	
2	99	92.5	180	4	Q9Y479	09y479 homo sapien	
3	99	92.5	210	4	Q9BU80	Q9bu80 homo sapien	
4	99	92.5	210	4	Q9UJB9	Q9ujb9 homo sapien	
5	62	57.9	301	5	Q8WSZ3	Q8wsz3 nephila clavipes	
6	62	57.9	550	5	Q86Z11	Q86z11 toxoplasma	
7	62	57.9	1039	10	Q8S0W4	Q8sw04 oryza sativa	
8	61.5	57.5	1953	5	Q9BIT7	Q9bit7 nephila ina	
9	60	56.1	465	4	Q86TH8	Q86th8 homo sapien	
10	60	56.1	926	11	Q8R554	Q8r554 mus musculus	
11	59	55.1	420	11	Q8CXY9	Q8cxy9 mus musculus	
12	59	55.1	538	11	Q8C278	Q8c278 mus musculus	
13	59	55.1	681	11	Q8C276	Q8c276 mus musculus	
14	58.5	54.7	563	5	Q9BITS5	Q9bits5 nephila ina	
15	58.5	54.7	566	5	Q19581	Q19581 caenorhabditis elegans	
16	58.5	54.7	569	5	Q9C522	Q9c522 caenorhabditis elegans	

RESULTS

RESULT 2

ID Q9Y479 PRELIMINARY;

AC 09Y479;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DR EMBL: AJ273978; CAB6945; 1. - .

KW Hypothetical protein.

FT NON_TTR 1 1

SEQUENCE 142 AA; 13895 MW; 2788E922AC4ACC7B CRC64;

SQ Query Match Length DB ID Description

1 107 100.0% 142 09ny13 Score 107; DB 4; Length 142;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPRGGAGAARASPGGGCAAPR 20

Db 17 RGPRGGAGAARASPGGGCAAPR 36

GN LAGE1.
OS Homo sapiens (Human).
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RX MEDLINE=9035556; PubMed=10399963;
RA Arnould C.A.; Van den Doe P.B.; Heemskerk B.; Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
unexpected translation product of LAGE-1.";
RT EMBL: AJ012835; CAA10196.1;-
RN [2]
SEQUENCE FROM N.A.
RA Aradhyu S.; Bardaro T.; Galgoczy P.; Yamagata T.; Esposito T.;
RA Patlak H.; Ciccodicola A.; Kenrick S.; Platzter M.; D'Urso M.;
RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35-
kb duplication involving the NEMO and the LAGE2 genes.";
RL Hum. Mol. Genet. 0:0-0(2001).
DR EMBL: AJ012834; CAA10194.1;-
DR EMBL: AF277115; AF277115.1;-
SQ SEQUENCE 180 AA; 18236 MW; 9077FAFF953543A25 CRC64;

Query Match 92.5%; Score 99; DB 4; Length 210;
Best Local Similarity 95.0%; Pred. No. 0.00013; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAPR 20
Db 43 RGPRGAGAARASGPGGGAPR 62

RESULT 3
ID Q9BU80 PRELIMINARY; PRT; 210 AA.
AC Q9BU80
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-OCT-2002 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DB Cancer/testis antigen 2.
OS Homo sapiens (Human).
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Straubberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002833; AAH02833.1;-
SQ SEQUENCE 210 AA; 21089 MW; 8FB5BF04FB04E8BE CRC64;

Query Match 92.5%; Score 99; DB 4; Length 210;
Best Local Similarity 95.0%; Pred. No. 0.00015; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAPR 20
Db 43 RGPRGAGAARASGPGGGAPR 62

RESULT 4
ID Q9UJB9 PRELIMINARY; PRT; 210 AA.
AC Q9UJB9
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2002 (TREMBLrel. 13, Last sequence update)
DE LAGE-1L protein.
GN Homo sapiens (Human).
OS

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Melanoma; PubMed=10399963;
RX MEDLINE=9935556; Van den Doe P.B.; Heemskerk B.; Schrier P.I.;
RA Aarnoudse C.A.; Van der Heijden C.A.; Van den Doe P.B.; Heemskerk B.; Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
unexpected translation product of LAGE-1.";
RT EMBL: AJ012835; CAA10196.1;-
SQ SEQUENCE 210 AA; 21060 MW; 1DD0B1829735B60A CRC64;

Query Match 92.5%; Score 99; DB 4; Length 210;
Best Local Similarity 95.0%; Pred. No. 0.00015; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAPR 20
Db 43 RGPRGAGAARASGPGGGAPR 62

RESULT 5
ID Q8WNSZ3 PRELIMINARY; PRT; 301 AA.
AC Q8WNSZ3
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DR EMBL: AAF32474.2.1;-
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 301 AA; 301396 MW; 8C69428B5684BD74 CRC64;

Query Match 57.9%; Score 62; DB 5; Length 301;
Best Local Similarity 66.7%; Pred. No. 6.1.; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GPRGAAARASGPGGAP 19
Db 130 GPGRGAAAARASGPGGYGP 147

RESULT 6
ID Q86P11 PRELIMINARY; PRT; 550 AA.
AC Q86P11
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DR J1P2.
OS Toxoplasma gondii.
OC Toxoplasma; Alveolata; Apicomplexa; Coccidia; Bimerida; Sarcocystidae;
OC Toxoplasma.
NCBI_TaxID=5811;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=RH;
RA Jiang L., Shu H., Luo S., Wu X., Cai L., Wang D., Zeng Q.;
RT "Immunological screening of Toxoplasma tachyzoite cDNA expression
libraries with serum from toxoplasma infected rats.";

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY208675; AAC043429.1; -;
SQ SEQUENCE 550 AA; 57890 MW; 18C71B4974BF0F34 CRC64;

Query Match Score 62; DB 5; Length 550;
Best Local Similarity 63.2%; Pred. No. 11;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 2 GPRGAGAARASGPGGGAPR 20
Db 524 GFORAGRAQADGIGACGPR 542

RESULT 7
Q8SOW4 PRELIMINARY; PRT; 1039 AA.
ID Q8SOW4 ID: Q8SOW4
AC Q8SOW4 AC: Q8SOW4
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
D3 OJ1014_G12.10 protein.
D3 OJ1014_G12.10 protein.
OS Oryza Sativa (japonica cultivar-group); Embryophyta; Tracheophyta;
OC Bokaryota; Viridiplantae; Streptophytina; Embryophytina; Trachophytina;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC Bhrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID:39947; [1]

SEQUENCE FROM N.A.
RC Nipponbare; STRAIN=cv. Nipponbare;
RA Sasaki T.; Matsumoto T.; Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
clone-OJ1014_G12.";
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
*RL EMBL; AAC03372; BAB83076.1; -.
DR Gramene; Q8SOW4; -.
DR InterPro; IPR007228; DUF390.
DR InterPro; IPR007321; transposase_2B.
DR Pfam; PP04094; DUF390.1.
DR Pfam; PP04095; Transposase_2B; 1.
SQ SEQUENCE 1039 AA; 11205 MW; A9A60FD34875DFD CRC64;

Query Match Score 62; DB 10; Length 1039;
Best Local Similarity 73.7%; Pred. No. 19;
Matches 14; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 3 PACAGAAARASG--PGGGAPR 19
Db 363 PRGGAAARASSRPGEGAP 381

RESULT 8
Q9BIT7 PRELIMINARY; PRT; 1953 AA.
ID Q9BIT7 ID: Q9BIT7
AC Q9BIT7 AC: Q9BIT7
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Major ampullate spidroin 2-like protein (Fragment).
OS Nephila inaurata madagascariensis.
OC Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.
OX NCBI_TaxID:115969; [1]

SEQUENCE FROM N.A.
RP MEDLINE=21119804; PubMed=11283372;
RA Gatesy J.; Hayashi C.; Motiuk D.; Woods J.; Lewis R.;
RT Fibroin Sequences;"
RL Science 291:2603-2605 (2001).
DR EMBL; AF350276; AAK3065.1; -.
FT NON_TER 1 1
FT NON_TER 1953 1953

SQ SEQUENCE 1953 AA; 159383 MW; C8224DADC043C3BD CRC64;
Query Match Score 61.5%; Best Local Similarity 68.4%; Matches 13; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
Qy 1 RGPRGAGAARASGPGGGAPR 19
Db 152 QGPRGPAGA-AAGGGYGP 169

RESULT 9
Q85TH8 PRELIMINARY; PRT; 465 AA.
ID Q85TH8 ID: Q85TH8
AC Q85TH8 AC: Q85TH8
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DB Adrenergic, alpha-2A-, receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606; [1]

SEQUENCE FROM N.A.
RN RP PROTEIN RECBP_F1_1; PRT; 465 AA.
RC TISSUE=Peripheral Nervous System;
RA Straubberg R.; RA
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL DR EMBL; BC050414; AAH50414.1; -.
DR Cintearial to membrane; IEA.
GO: GO:0016021; Cintearial to membrane; IEA.
DR GO: GO:0004872; C receptor activity; IEA.
DR GO: GO:0001584; C:Rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P-G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPRO00276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPROTRHOOPEN.
DR PROSITE; PS00237; G PROTEIN RECBP_F1_1;
DR PROSITE; PS50262; G PROTEIN RECBP_F1_2;
DR Receptor; KW SQ SEQUENCE 465 AA; 50646 MW; 585-E576149BDB696 CRC64;

Query Match Score 60; Best Local Similarity 63.6%; Matches 14; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
PRT; 465 AA. Length 465;

Q8R554 PRELIMINARY; PRT; 926 AA.
ID Q8R554 ID: Q8R554
AC Q8R554 AC: Q8R554
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DB Cezanne 2 Protein.
GN AJ430384 OR CEZANN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090; [1]

SEQUENCE FROM N.A.
RN RP STRAIN=C57 BL/6;
RC Evans P.C.; Coddwell W.J.; Kilshaw P.J.;
RA "Isolation of a novel murine gene, Cezanne 2,";
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ410384; CAB23048.1; -.
DR MGI; MGI:2158565; AJ430384.
DR InterPro; IPR003323; OTU.
DR PROSITE; PS50802; OTU. 1.

SQ	SEQUENCE	926 AA;	100795 MW;	4D6BD05A0410BED9 CRC64;	
	Query Match	56.1%;	Score 60;	DB 11;	Length 926;
	Best Local Similarity	60.0%;	Pred. No. 30;		
	Matches 12;	Conservative 1;	Mismatches 7;	Indels 0;	Gaps 0;
Qy	1	RGRPGAGARASGPGGCCPR	20		
Db	739	RAARANGGAASPGPGGARR	758		
RESULT 11					
ID	QBCBY9	PRELIMINARY;	PRT;	420 AA.	
AC	QBCBY9;				
DT	01-MAR-2003	(TREMBLrel. 23; Created)			
DT	01-MAR-2003	(TREMBLrel. 23; Last sequence update)			
DT	01-OCT-2003	(TRIMBRELrel. 25; Last annotation update)			
DE	Eph receptor A5.				
OS	Mus musculus (Mouse).				
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID	10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Diencephalon;				
RX	MEDLINE=22354683; PubMed=12466851;				
RA	The FANTOM Consortium,				
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";				
RT	Nature 420:563-573 (2002).				
DR	EMBL: AX034289; BAC28660.1; -.				
DR	GO: GO:0016020; C:membrane; IBA.				
DR	GO: GO:005224; F:ephrin receptor activity; IBA.				
DR	GO: GO:0005003; F:protein amino acid phosphorylation; IBA.				
DR	GO: GO:0006468; P:transmembrane receptor protein tyrosine kinase; IBA.				
DR	InterPro: IPR006209; EGF like.				
DR	InterPro: IPR001090; Ephrin receptor.				
DR	InterPro: IPR001426; Gal-bind like.				
DR	InterPro: IPR006879; Yak3 receptor.				
DR	Pfam: PF01404; EPH lbd; 1.				
DR	ProDom: PD001495; Ephrin receptor; 1.				
DR	SMART; SM00615; EPH lbd; 1.				
DR	PROSITE; PS001186; EGP_2; 1.				
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.				
DR	PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.				
DR	SEQUENCE 420 AA; 46434 MW; 88604DE8P73C98D4 CRC64;				
DR	Best Local Similarity 61.9%;	Pred. No. 19;	Score 59;	DB 11;	Length 420;
DR	Matches 13; Conservative 0;	Mismatches 6;	Indels 2;	Gaps 1;	
Qy	2	GPRGAGAARASGPGGG--APR 20			
Db	5	GPRGAGHRRTQGRGGDDTPR 25			
RESULT 12					
ID	QBC278	PRELIMINARY;	PRT;	538 AA.	
AC	QBC278;				
DT	01-MAR-2003	(TREMBLrel. 23; Created)			
DT	01-MAR-2003	(TREMBLrel. 23; Last sequence update)			
DT	01-OCT-2003	(TRIMBRELrel. 25; Last annotation update)			
DE	Eph receptor A5.				
OS	Mus musculus (Mouse).				
OC	Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID	10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RI	Nature 420:563-573 (2002);				
RC	STRAIN=C57BL/6J; TISSUE=Olfactory brain;				
RA	MEDLINE=22354683; PubMed=12466851;				
RA	The FANTOM Consortium,				
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";				
RT	InterPro: IPR006209; EGP like.				
DR	InterPro: IPR01090; Ephrin receptor.				
DR	InterPro: IPR003962; Gal-bind like.				
DR	InterPro: IPR0016020; C:membrane; IBA.				
DR	GO: GO:0005524; P:ATP binding; IBA.				
DR	GO: GO:0050009; P:ephrin receptor activity; IBA.				
DR	GO: GO:0006468; P:protein amino acid phosphorylation; IBA.				
DR	GO: GO:0007167; P:transmembrane receptor protein tyrosine kinase; IBA.				
DR	SEQUENCE FROM N.A.				
QBC278	PRELIMINARY;	PRT;	538 AA.		
AC	QBC278;				
DT	01-MAR-2003	(TREMBLrel. 23; Created)			
DT	01-MAR-2003	(TREMBLrel. 23; Last sequence update)			
DT	01-OCT-2003	(TRIMBRELrel. 25; Last annotation update)			
DE	Eph receptor A5.				
OS	Mus musculus (Mouse).				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID	10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				

DR InterPro; IPR001426; YKase_receptorv.
 DR PFam; PF01446; EPH_1bd; 1.
 DR PRINTS; PR00014; FNTPEIIL.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR SMART; SM00060; EPH_1bd; 1.
 DR PROSITE; PS001186; EGF_2; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V-1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V-2; 1.
 SQ SEQUENCE 681 AA; 75336 MW; _92B5187AB78BE722 CRC64;

Query Match 55.1%; Score 59; DB 11; Length 681;
 Best Local Similarity 61.9%; Pred. No. 30;
 Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy	2 GPRGAGAARASPGGG-APR 20
Ds	5 GPRGAHRRRTQGRGGDDTPR 25

RESULT 14
 Q9BITS ID Q9BITS PRELIMINARY; PRT; 563 AA.
 AC Q9BITS; Q9BITS;
 DT 01-JUN-2001 (TREMBLref; 17, Created)
 DT 01-JUN-2001 (TREMBLref; 17, Last sequence update)
 DT 01-JUN-2003 (TREMBLref; 24, Last annotation update)
 DE Major ampullae spidroin 2 (Fragment).
 GN MASP2.
 OS Nephila inaurata madagascariensis.
 OC Araneomorphae; Entelegynae; Araneoidea; Araneida; Arachnida; Araneae;
 OC NCBITaxonID=115969;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21179804; PubMed=11283172;
 :R2 Gatesy J., Hayashi C., Morriuk D., Woods J., Lewis R.; Spider Silk
 :R2 Extreme Diversity, Conservation, and Convergence of Spider Silk
 RT Fibroin Sequences;
 RL Science 291:2603-2605 (2001).
 DR EMBL; AF350278; ARKS0607.1; -.
 FT NON_TER 1 1
 PT NON_TER 563 563
 SQ SEQUENCE 563 AA; 48361 MW; 0AEAD885304B886B CRC64;

Query Match 54.7%; Score 58.5%; DB 5; Length 563;
 Best Local Similarity 59.1%; Pred. No. 29;
 Matches 13; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

Qy	1 RGPRGAG-~NARASPGGGAP 19
Ds	406 QEPGAGCSAAAAAAGGGYGP 427

RESULT 15
 Q19581 ID Q19581 PRELIMINARY; PRT; 566 AA.
 AC Q19581;
 DT 01-NOV-1996 (TREMBLref; 01, Created)
 DT 01-NOV-1996 (TREMBLref; 01, Last sequence update)
 DT 01-OCT-2003 (TREMBLref; 25, Last annotation update)
 DE F18H3_3b protein.
 GN F18H3_3 OR F18H3_3B.
 OS Caenorhabditis elegans.
 OC Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peioderinae; Caenorhabditidae.
 RN [1]
 RP SEQUENCE FROM N.A.
 :R2 Submitted (JUL-1995) to the TREMBL/GenBank/DDJB databases.
 RA Coles L.;